

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:24:18 ; Search time 2566.56 Seconds
(without alignments)
11346.531 Million cell updates/sec

Title: US-09-497-957-9_COPY_465_1065

Perfect score: 601
Sequence: 1 CAGATGTGGTGCAGCTGAG.....GGAAGAGCAGAGATATACGT 601

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	100.0	860	9 AY205604	AY205604 Homo sapi
2	601	100.0	1200	9 AF115265	AF115265 Homo sapi
3	601	100.0	1280	9 HSA249335	AJ249335 Homo sapi
4	601	100.0	1317	6 AX407339	AX407339 Sequence
5	601	100.0	1440	6 AR117793	AR117793 Sequence
6	601	100.0	1440	6 AR117794	AR117794 Sequence
7	601	100.0	1440	6 AR117795	AR117795 Sequence
8	601	100.0	1440	6 AR117796	AR117796 Sequence
9	601	100.0	1440	6 AR149463	AR149463 Sequence
10	601	100.0	1440	6 AR149464	AR149464 Sequence
11	601	100.0	1440	6 AR149465	AR149465 Sequence
12	601	100.0	1440	6 AR149466	AR149466 Sequence
13	601	100.0	2506	6 AR199238	AR199238 Sequence
14	601	100.0	2506	6 AR275757	AR275757 Sequence
15	601	100.0	2716	6 CO717466	CO717466 Sequence
16	601	100.0	2727	9 HSU50319	U60319 Homo sapien
17	533	88.7	1123	9 BC074721	BC074721 Homo sapi
18	507	84.4	1045	9 AF079407	AF079407 Homo sapi
19	504.4	83.9	823	9 AF079408	AF079408 Homo sapi

20	504.4	83.9	1085	9 HSA249336	AJ249336 Homo sapi
21	486.8	81.0	686	9 AF144240	AF144240 Homo sapi
22	484.2	80.6	1320	4 AY007541	AY007541 Ceratopthe
23	481	80.0	1319	4 AY007544	AY007544 Rhinocero
24	481	80.0	1320	4 AY007543	AY007543 Dicerorhi
25	477.8	79.5	2332	4 AY007542	AY007542 Dicerorhi
26	410.4	68.3	781	9 AF079409	AF079409 Homo sapi
27	377	62.7	789	10 AF008587	AF008587 Rattus no
28	377	62.7	1706	10 RNERHAEM	AJ001517 Rattus no
29	377	62.7	3520	10 BC070942	BC070942 Rattus no
30	357.4	59.5	1529	10 MM066849	U66849 Mus musculu
31	337.4	56.1	819	10 AF176534	AF176534 Rattus no
32	320.4	53.3	492	9 AF144241	AF144241 Homo sapi
33	286.6	47.7	489	9 AF144239	AF144239 Homo sapi
34	277	46.1	874	9 HSHLAH2	Y09800 H. sapiens H
35	277	46.1	5982	6 AX701831	AX701831 Sequence
36	277	46.1	10825	6 AR117789	AR117789 Sequence
37	277	46.1	10825	6 AR117790	AR117790 Sequence
38	277	46.1	10825	6 AR117791	AR117791 Sequence
39	277	46.1	10825	6 AR117792	AR117792 Sequence
40	277	46.1	10825	6 AR149459	AR149459 Sequence
41	277	46.1	10825	6 AR149460	AR149460 Sequence
42	277	46.1	10825	6 AR149461	AR149461 Sequence
43	277	46.1	10825	6 AR149462	AR149462 Sequence
44	277	46.1	11214	9 AF447807	AF447807 Pan trogl
45	277	46.1	12146	6 AR199263	AR199263 Sequence

ALIGNMENTS

RESULT 1	AY205604	Homo sapiens hemochromatosis (HFE) mRNA, partial cdb.	860 bp	mRNA	linear	PRI 03-MAR-2003
LOCUS	AY205604					
DEFINITION	AY205604					
ACCESSION	AY205604.1	GI:28800981				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

FEATURES						
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/db_xref="taxon:9606"						
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<1..808						
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KDQKPMDAKEFPBKDVLPNGDGTYYQGYITLAVPPGEEQRYTCQVHEPGLDQPLIVINE
PSPSGTLVIGVISGIAVFFVILLFIFILRRKQSGAMGHYLAERE"

ORIGIN	Query Match	100.0%;	Score 601;	DB 9;	Length 860;	
	Best Local Similarity	100.0%;	Pred. No. 3.2e-160;			
	Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCACTGTTGAC	60			
Db	5	CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCACTGTTGAC	64			
QY	61	TTCTGGACTATTATGGAATAATCAACACACAGCAAGAGTCCACACCTTCGAGGTCATC	120			
Db	65	TTCTGGACTATTATGGAATAATCAACACACAGCAAGAGTCCACACCTTCGAGGTCATC	124			
QY	121	CTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180			
Db	125	CTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	184			
QY	181	GGSCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG	240			
Db	185	GGSCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG	244			
QY	241	GCCTGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC	300			
Db	245	GCCTGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC	304			
QY	301	TACTTGGAGGAGGACTGCCTCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGTGTT	360			
Db	305	TACTTGGAGGAGGACTGCCTCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGTGTT	364			
QY	361	TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGACC	420			
Db	365	TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGACC	424			
QY	421	ACTCTAGGTGTGCGGCCTTGAATACTACTACCCCAAGCAATCATCATGAGTGGCTGAAG	480			
Db	425	ACTCTAGGTGTGCGGCCTTGAATACTACTACCCCAAGCAATCATCATGAGTGGCTGAAG	484			
QY	481	GATAAGCAGCAATGATGCAAGGAGTTTGAACCTTAAAGACCTATTTCGCCAATGGGGAT	540			
Db	485	GATAAGCAGCAATGATGCAAGGAGTTTGAACCTTAAAGACCTATTTCGCCAATGGGGAT	544			
QY	541	GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG	600			
Db	545	GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG	604			
QY	601	T 601				
Db	605	T 605				

RESULT 2
AF115265
LOCUS
DEFINITION
Homo sapiens hemochromatosis termination variant terE6 (HFE) mRNA,
complete cds.
ACCESSION
AF115265
VERSION
AF115265.1 GI:11094314
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1200)
AUTHORS
Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y.,
David,V.T. and Mosser,J.
TITLE
The HFE gene undergoes alternate splicing processes
JOURNAL
Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
MEDLINE
20448010
PUBMED
11001625
REFERENCE
2 (bases 1 to 1200)

AUTHORS	Thenie,A., Orhant,M. and Mosser,J.
TITLE	Direct Submission
JOURNAL	Submitted (17-DEC-1998) UPR 41 CNRS, Faculte de Medecine, 2, av du Pr. Bernard, Rennes 35043, France
FEATURES	Location/Qualifiers
source	1..1200
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	/chromosome="6"
	/map="6p22"
gene	1..1200
	/gene="HFE"
CDS	12..1058
	/gene="HFE"
	/codon_start=1
	/product="hemochromatosis termination variant terE6"
	/protein_id="ANG29572.1"
	/db_xref="GI:11094315"
	/translation="MGRARPALLLMLLQTLAVLQGRLLRSHLSHLVFMGASEQDILGL SLFEALGYDDQLFVYDHERRVERPTPVSSRISSQMWLQSLKGMDFMTVDF WTIMENHNKESHITLQVILGCEQEDNSTEGYKYGVDQDLDFCPLDWRAAEP RAWPTKLEWRHKIRARONRAYLERDPAQLQLELGRVLDQDQVPLVKVTHVTS SVTTLRCALNYVPONITMKWLKDKPMDAKEFBPKDVLPGDGTQGMWITLAVPGE BQRYTCQVHEPGLDQPLIVIEWEPPSPSGTLVIGVISGIAVFFVILLFIFILRRKQG SRGAMGHYVLAERE"
ORIGIN	
	Query Match 100.0%; Score 601; DB 9; Length 1200;
	Best Local Similarity 100.0%; Pred. No. 3.3e-160;
	Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCACTGTTGAC 60
Db	255 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCACTGTTGAC 314
QY	61 TTCTGGACTATTATGGAATAATCACAAACACAGCAAGGAGTCCACACCTTCGAGGTCATC 120
Db	315 TTCTGGACTATTATGGAATAATCACAAACACAGCAAGGAGTCCACACCTTCGAGGTCATC 374
QY	121 CTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT 180
Db	375 CTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT 434
QY	181 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGACAGACCCAGG 240
Db	435 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGACAGACCCAGG 494
QY	241 GCCTGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 300
Db	495 GCCTGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 554
QY	301 TACCTGGAGAGGAGCTGCCCTTCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGTGTT 360
Db	555 TACCTGGAGAGGAGCTGCCCTTCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGTGTT 614
QY	361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db	615 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 674
QY	421 ACTCTAGGTGTGCGGCCTTGAATACTACTACCCCAAGCAATCATCATGAGTGGCTGAAG 480
Db	675 ACTCTAGGTGTGCGGCCTTGAATACTACTACCCCAAGCAATCATCATGAGTGGCTGAAG 734
QY	481 GATAAGCAGCAATGAGTGCAGAGGAGTTTGAACCTTAAAGACCTATTTCGCCAATGGGGAT 540
Db	735 GATAAGCAGCAATGAGTGCAGAGGAGTTTGAACCTTAAAGACCTATTTCGCCAATGGGGAT 794
QY	541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600
Db	795 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 854
QY	601 T 601

Db 855 T 855

RESULT 3
HSA249335 1280 bp mRNA linear PRI 02-JUL-2004
LOCUS Homo sapiens mRNA for hemochromatosis protein (HFE gene) splice
DEFINITION variant 1.
ACCESSION AJ249335
VERSION AJ249335.1 GI:15485418
KEYWORDS alternative splicing; hemochromatosis protein; HFE gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Sanchez, M., Bruguera, M., Rodas, J. and Oliva, R.
TITLE Complete characterization of the 3' region of the human and mouse hereditary hemochromatosis HFE gene and detection of novel splicing forms
JOURNAL Blood Cells Mol. Dis. 27 (1), 35-43 (2001)
MEDLINE 21257661
PUBMED 11358357

REFERENCE
AUTHORS Oliva, R.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN

FEATURES
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1. .1280
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1. .1280
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161. .1138
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ERDCPAQLQOLLELGRVLDQVPPVLTHTVHTSVTLRLCALNYPONTIMRWLK
DKQPMDAKEFPKVDLPNGEGTYQGMITLAVPEGEQRYTCQVHEPLDQPLIVIEP
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ORIGIN
Query Match 100.0%; Score 601; DB 9; Length 1280;
Best Local Similarity 100.0%; Pred. No. 3.3e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 60
Db |
335 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 394
QY 61 TTCTGACTATTATGAAATATCAACACAGCAAGAGTCCACACCTCGCAGGTGATC 120
Db |
395 TTCTGACTATTATGAAATATCAACACAGCAAGAGTCCACACCTCGCAGGTGATC 454
QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
Db |
455 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 514

QY 181 GGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 240
Db |
515 GGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 574
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTCCGGCCAGGCAAGACAGGGCC 300
Db |
575 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTCCGGCCAGGCAAGACAGGGCC 634
QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCACAGAGTTGCTGGAGTGGGGAGAGGTGTT 360
Db |
635 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCACAGAGTTGCTGGAGTGGGGAGAGGTGTT 694
QY 361 TTGGACCAACAAGTGGCTCTCTTTGGTGAAGGTGCACATCATGTGACCTCTTCACTGACCC 420
Db |
695 TTGGACCAACAAGTGGCTCTCTTTGGTGAAGGTGCACATCATGTGACCTCTTCACTGACCC 754
QY 421 ACTTACCGGTGTCGGGCTTGAACCTACTACCCAGAAACATCACCATTGAAGTGGCTGAAG 480
Db |
755 ACTTACCGGTGTCGGGCTTGAACCTACTACCCAGAAACATCACCATTGAAGTGGCTGAAG 814
QY 481 GATAAGCGCAATGATGCCAAGGAGTTTGAACCTTAAAGACGTTATTTGCCCAATGGCGAT 540
Db |
815 GATAAGCGCAATGATGCCAAGGAGTTTGAACCTTAAAGACGTTATTTGCCCAATGGCGAT 874
QY 541 GGCAGCTTACCGGCTGGGATTAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 600
Db |
875 GGCAGCTTACCGGCTGGGATTAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 934
QY 601 T 601
Db |
935 T 935

RESULT 4
AX407339 1317 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 1 from Patent WO0224929.
DEFINITION AX407339
ACCESSION AX407339
VERSION AX407339.1 GI:21440046
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Ehrlich, R., Rotem-Yehudar, R. and Laham, N.
TITLE A soluble beta 2 microglobulin (betazm)/hfe monochain for biotechnological and therapeutic applications
JOURNAL Patent: WO 0224929-A 1 28-MAR-2002;
Ramat University Authority for Applied Research & Industrial Dev LTD. (II)

FEATURES
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ORIGIN

Query Match	100.0%;	Score 601;	DB 6;	Length 1317;
Best Local Similarity	100.0%;	Pred. No. 3.3e-160;		
Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC	60	
Db	580	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC	639	
QY	61	TTCTGGACTATTATGAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	120	
Db	640	TTCTGGACTATTATGAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	699	
QY	121	CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180	
Db	700	CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	759	
QY	181	GGGACGACACCTTGAATTCCTGCTGACACACTGGAATGAGAGCAGACAGCCAGG	240	
Db	760	GGGACGACACCTTGAATTCCTGCTGACACACTGGAATGAGAGCAGACAGCCAGG	819	
QY	241	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTCCGGCCAGGAGCAACAGG	300	
Db	820	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTCCGGCCAGGAGCAACAGG	879	
QY	301	TACCTGGAGAGGACTGCGCTTGCACAGCTGCAGAGTTCCTGGAGTGGGGAGAGTGT	360	
Db	880	TACCTGGAGAGGACTGCGCTTGCACAGCTGCAGAGTTCCTGGAGTGGGGAGAGTGT	939	
QY	361	TTGGACCAACAAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	420	
Db	940	TTGGACCAACAAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	999	
QY	421	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	480	
Db	1000	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	1059	
QY	481	GATAAGCAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	540	
Db	1060	GATAAGCAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	1119	
QY	541	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGAGATATACG	600	
Db	1120	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGAGATATACG	1179	
QY	601	T 601		
Db	1180	T 1180		
RESULT 5				
LOCUS	AR117793	1440 bp	DNA	linear
DEFINITION	Sequence 9 from patent US 6140305.			PAT 16-MAY-2001
ACCESSION	AR117793			
VERSION	AR117793.1	GI:14098699		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1440)			
AUTHORS	Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.			
TITLE	Hereditary hemochromatosis gene products			
JOURNAL	Patent: US 6140305-A 9 31-OCT-2000;			
FEATURES	Location/Qualifiers			
source	1..1440			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
ORIGIN				
Query Match	100.0%;	Score 601;	DB 6;	Length 1440;
Best Local Similarity	100.0%;	Pred. No. 3.4e-160;		
Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC	60	
Db	465	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC	524	
QY	61	TTCTGGACTATTATGAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	120	
Db	525	TTCTGGACTATTATGAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	584	
QY	121	CTGGGCTGTGAATCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180	
Db	585	CTGGGCTGTGAATCAAGAGACACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT	644	
QY	181	GGGACGACACCTTGAATTCCTGCTGACACACTGGAATGAGAGCAGACAGCCAGG	240	
Db	645	GGGACGACACCTTGAATTCCTGCTGACACACTGGAATGAGAGCAGACAGCCAGG	704	
QY	241	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTCCGGCCAGGAGCAACAGG	300	
Db	705	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTCCGGCCAGGAGCAACAGG	764	
QY	301	TACCTGGAGAGGACTGCGCTTGCACAGCTGCAGAGTTCCTGGAGTGGGGAGAGTGT	360	
Db	765	TACCTGGAGAGGACTGCGCTTGCACAGCTGCAGAGTTCCTGGAGTGGGGAGAGTGT	824	
QY	361	TTGGACCAACAAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	420	
Db	825	TTGGACCAACAAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	884	
QY	421	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	480	
Db	885	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	944	
QY	481	GATAAGCAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	540	
Db	945	GATAAGCAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	1004	
QY	541	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGAGATATACG	600	
Db	1005	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGAGATATACG	1064	
QY	601	T 601		
Db	1065	T 1065		
RESULT 6				
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DEFINITION	Sequence 10 from patent US 6140305.			PAT 16-MAY-2001
ACCESSION	AR117794			
VERSION	AR117794.1	GI:14098700		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1440)			
AUTHORS	Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.			
TITLE	Hereditary hemochromatosis gene products			
JOURNAL	Patent: US 6140305-A 10 31-OCT-2000;			
FEATURES	Location/Qualifiers			
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Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy 301 TACTTGGAGAGGACTGCTCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGGAGAGGTGTT 360
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Qy 601 T 601
Db 1065 T 1065

RESULT 7
AR117795
LOCUS 1440 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6140305.
ACCESSION AR117795
VERSION AR117795.1 GI:14098701
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1440)
AUTHORS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 11 31-OCT-2000;
FEATURES Location/Qualifiers
source
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ORIGIN
Query Match 100.0%; Score 601; DB 6; Length 1440;
Best Local Similarity 100.0%; Pred. No. 3.4e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGATGTGGCTGAGTCAAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 60
Db 465 CAGATGTGGCTGAGTCAAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 524
Qy 61 TTCTGGACTATTATGGAATAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTATC 120

Db 525 TTCTGGACTATTATGGAATAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTATC 584
Qy 121 CTGGCTGTGAATGCAAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
Db 585 CTGGCTGTGAATGCAAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644
Qy 181 GGGCAGGACCACTTGAATTTCTGCTTGACACACTGATTTGGAGAGCAGCAGAACCCAGG 240
Db 645 GGGCAGGACCACTTGAATTTCTGCTTGACACACTGATTTGGAGAGCAGCAGAACCCAGG 704
Qy 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 300
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Qy 301 TACTTGGAGAGGACTGCTCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGGAGAGGTGTT 360
Db 765 TACTTGGAGAGGACTGCTCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGGAGAGGTGTT 824
Qy 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 884
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Qy 601 T 601
Db 1065 T 1065

RESULT 8
AR117796
LOCUS 1440 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 12 from patent US 6140305.
ACCESSION AR117796
VERSION AR117796.1 GI:14098702
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1440)
AUTHORS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 12 31-OCT-2000;
FEATURES Location/Qualifiers
source
1. .1440
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ORIGIN
Query Match 100.0%; Score 601; DB 6; Length 1440;
Best Local Similarity 100.0%; Pred. No. 3.4e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGATGTGGCTGAGTCAAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 60
Db 465 CAGATGTGGCTGAGTCAAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 524
Qy 61 TTCTGGACTATTATGGAATAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTATC 120
Db 525 TTCTGGACTATTATGGAATAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTATC 584

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DB	645	GGGCGAGGCACCTTTGAATTTTCGCCCTGCACACTGTGGATTGGAGAGCAGCAAAACCACGG	704
QY	241	GCCTGGCCCCACAAGCTGGAGTGGGAAAGGCACAAGATTCCGGGCCACGCAGAACAGGGCCC	300
DB	705	GCCTGGCCCCACAAGCTGGAGTGGGAAAGGCACAAGATTCCGGGCCACGCAGAACAGGGCCC	764
QY	301	TACTTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGATTGTCTGGAGCTGGGGAGAGGTTT	360
DB	765	TACTTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGATTGTCTGGAGCTGGGGAGAGGTTT	824
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DB	825	TTGGNCCAACAAGTGCCCTTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACC	884
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DB	885	ACTCTACGGTGTGGGGCCTTGAACTTACTTACCCCCAGAACATCATCATGAAGTGGCTCAAG	944
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QY	541	GGGACCTTACCAAGGCTGGATAAACCCTTGGCTGTACCCCTGGGGGAAGACGAGAGATATACG	600
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Db	705	GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCACAAGATTTCGGCCAGGCAGACAGAGGCC	764
Qy	301	TACCTGGAGAGGAGCTGCCCTGTCACAGCTCCAGCAGTGTCTGGAGCTGGGGAGAGGTGTT	360
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Qy	361	TTGGACCAACAAGTGCTCTCTTTGGTGAAGGTGCACATCATGTGACCTCTTCAGTGACC	420
Db	825	TTGGACCAACAAGTGCTCTCTTTGGTGAAGGTGCACATCATGTGACCTCTTCAGTGACC	884
Qy	421	ACTCTACGGTGTGGGGCTTGAACACTACTACCCCCAGAAACATCAACATGAAGTGGCTGAAG	480
Db	885	ACTCTACGGTGTGGGGCTTGAACACTACTACCCCCAGAAACATCAACATGAAGTGGCTGAAG	944
Qy	481	GATAAGCAGCAATGGATGCAAGAGGTTCGAACCTTAAGACGTATTTGCCAATGGGGAT	540
Db	945	GATAAGCAGCAATGGATGCAAGAGGTTCGAACCTTAAGACGTATTTGCCAATGGGGAT	1004
Qy	541	GGGACCTTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAGCAGACATATACG	600
Db	1005	GGGACCTTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAGCAGACATATACG	1064
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Db	1065	T 1065	
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
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Best Local Similarity			
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Qy	61	TTCTGCACTATTATGAAATATCACACCAAGAGAGTCCACACCTTCGAGGTCATC	120
Db	525	TTCTGCACTATTATGAAATATCACACCAAGAGAGTCCACACCTTCGAGGTCATC	584
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Db	585	CTGGGCTGTGAAATGCAAGAAGACACAGTACCGAGGGCTACTCGAAGTACGGGTATGAT	644
Qy	181	GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGCAGAAACCCAGG	240
Db	645	GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGCAGAAACCCAGG	704

QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACNAGATTTCGGGCCAGGCAGAACAGGGCC 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACNAGATTTCGGGCCAGGCAGAACAGGGCC 764
QY 301 TACCTGGAGAGGAGCTGCCCTCGACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 360
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QY 361 TTGGACCAACAAGTGCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
DB 825 TTGGACCAACAAGTGCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
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DB 945 GATAAGCAGCAATGATGCCAAGAGTTTGAACCTTAAAGAGCTATTGGCCCAATGGGAT 1004
QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600
DB 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064
QY 601 T 601
DB 1065 T 1065

RESULT 13
AR199238
LOCUS AR199238 2506 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6355425.
ACCESSION AR199238
VERSION AR199238.1 GI:20249312
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2506)
AUTHORS Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
TITLE Mutations associated with iron disorders
JOURNAL Patent: US 6355425-A 1 12-MAR-2002;
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Query Match 100.0%; Score 601; DB 6; Length 2506;
Best Local Similarity 100.0%; Pred. No. 3.5e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 844 T 844

RESULT 14
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LOCUS AR275757 2506 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6509442.
ACCESSION AR275757
VERSION AR275757.1 GI:29709314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2506)
AUTHORS Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.
TITLE Mutations associated with iron disorders
JOURNAL Patent: US 6509442-A 1 21-JAN-2003;
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Best Local Similarity 100.0%; Pred. No. 3.5e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTCTGGACTATTATGAAATCACAACCAAGAGTCCACACCTTCAGGTCATC 120
DB 304 TTCTGGACTATTATGAAATCACAACCAAGAGTCCACACCTTCAGGTCATC 363
QY 121 CTGGGCTGTGAAATGCAAGAGACAAACAGTCCGAGGGCTACTGGAAGTACGGGTATGAT 180
DB 364 CTGGGCTGTGAAATGCAAGAGACAAACAGTCCGAGGGCTACTGGAAGTACGGGTATGAT 423
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DB 424 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAGG 483
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACNAGATTTCGGGCCAGGCAGAACAGGGCC 300
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QY 301 TACCTGGAGAGGAGCTGCCCTCGACAGCTGCAGCAGTTCGGAGCTGGGGAGAGGTGTT 360
DB 544 TACCTGGAGAGGAGCTGCCCTCGACAGCTGCAGCAGTTCGGAGCTGGGGAGAGGTGTT 603

Qy	361	TTGGACCAACAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC	420
Db	604	TTGGACCAACAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC	663
Qy	421	ACTCTACGGTGTGGGGCTTGAACCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG	480
Db	664	ACTCTACGGTGTGGGGCTTGAACCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG	723
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Db	724	GATTAAGCAGCCAAATGGATGCCAAGGAGTTCGAACTCTAAAGACGTATTGCCCAATGGGGAT	783
Qy	541	GGGACCTACCAAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGACGAGATATACG	600
Db	784	GGGACCTACCAAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGACGAGATATACG	843
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RESULT 15
LOCUS      CQ717466                2716 bp    DNA
DEFINITION Sequence 3400 from Patent WO02068579.
ACCESSION  CQ717466
VERSION     CQ717466.1  GI:42278323
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE       Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL     Patent: WO 02068579-A 3400 06-SEP-2002;
            PE Corporation (NY) (US)
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Query Match	100.0%	Score 601;	DB 6;	Length 2716;
Best Local Similarity	100.0%;	Pred. No. 3.6e-160;		
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Qy	61	TTCTGGACTATTATGGAAAAATCAAAACACAGCAAGGAGTCCCAACACCTTCGAGGTCATC	120	
Db	525	TTCTGGACTATTATGGAAAAATCAAAACACAGCAAGGAGTCCCAACACCTTCGAGGTCATC	584	
Qy	121	CTGGCGTGTGAAATGCAAGAAGACAAAGTACCGAGGGCTACTGGAAAGTACGGGTATGAT	180	
Db	585	CTGGCGTGTGAAATGCAAGAAGACAAAGTACCGAGGGCTACTGGAAAGTACGGGTATGAT	644	
Qy	181	GGCAGGACACACCTTGTAATTTCTGCCCTTGACACACTGGATTGGAGAGCAGCAGAACCCAGG	240	
Db	645	GGCAGGACACACCTTGTAATTTCTGCCCTTGACACACTGGATTGGAGAGCAGCAGAACCCAGG	704	
Qy	241	GCCTGGCCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCCGGGCCAGGCAGAACCGGCC	300	
Db	705	GCCTGGCCCCACCAAGCTGGAGTGGGAAAGGCACAAGATTCCGGGCCAGGCAGAACCGGCC	764	
Qy	301	TACCTGGAGAGGGACTCCCTGCAACAGCTGCAGCGATTGCTGGAGCTGGGGAGAGGTGTT	360	
Db	765	TACCTGGAGAGGGACTCCCTGCAACAGCTGCAGCGATTGCTGGAGCTGGGGAGAGGTGTT	824	

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

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7: Geneseqn2002bs:*

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12: Geneseqn2004as:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	601	100.0	1439	10	ADG87269 Hereditar
7	601	100.0	1440	2	AAT96691 Hereditar
8	601	100.0	1440	5	AAC68430 Human her
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13	601	100.0	2727	2	AAV23525 Haemochro
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28	277	46.1	5749	12	ADJ30485	Adj30485 Human mus
29	277	46.1	5982	8	ABV93934	Abv93934 Human col
30	277	46.1	10824	10	ADG87338	Adg87338 Hereditar
31	277	46.1	10824	10	ADG87266	Adg87266 Hereditar
32	277	46.1	10825	2	AAT96690	Aat96690 Hereditar
33	277	46.1	10825	5	AAC68426	Aac68426 Human her
34	277	46.1	10825	5	AAC68427	Aac68427 Human her
35	277	46.1	10825	5	AAC68428	Aac68428 Human her
36	277	46.1	10825	5	AAC68425	Aac68425 Human her
37	277	46.1	10825	10	ADG87262	Adg87260 Hereditar
38	277	46.1	10825	10	ADG87262	Adg87262 Hereditar
39	277	46.1	10825	10	ADG87264	Adg87264 Hereditar
40	277	46.1	12146	3	AA96794	Aaa96794 Genomic D
41	277	46.1	235033	2	AAV57926	Aav57926 Hereditar
42	277	46.1	237326	2	AAV57903	Aav57903 Hereditar
43	260.6	43.4	596	4	AAI63897	Aai63897 Human pol
44	260.6	43.4	596	12	ADM24448	Adm24448 Human PRO
45	232	38.6	359	2	AAX16055	Aax16055 Hereditar

ALIGNMENTS

RESULT 1

ABK49917

ID ABK49917 standard; cDNA; 1317 BP.

AC ABK49917;

DT 15-JUL-2002 (first entry)

DE DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.

Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia; iron absorption regulator; intracellular iron absorption; lung injury; haemochromatosis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; TFR; brain tumour; cancer; oxidative stress disorder; tissue damage; vascular disease; inflammation; atherosclerosis; autoimmune disease; inflammatory condition; gene; ss.

OS Homo sapiens.

XX Location/Qualifiers

XX Key 1..1317

XX CDS /*tag= a

XX FT /product= "beta2M/HFE monochain"

XX WO200224929-A2.

XX 28-MAR-2002.

XX 24-SEP-2001; 2001WO-US0299873.

XX 22-SEP-2000; 2000US-0234843P.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX (MCIN/) MCINNIS P.

XX Ehrlich R, Rotem-Yehudar R, Laham N;

XX WPI; 2002-383192/41.

XX P-PSDB; AAU80035.

Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by a linker

PT peptide.
XX
PS Example 2; Fig 2; 77pp; English.
XX
CC The invention relates to a soluble polypeptide (I) of beta 2
CC microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC analogue or active fragment), linked to alpha1-alpha3 domains of human
CC HFE (a central regulator of iron absorption; undefined), or its analogue
CC or active fragment, by a flexible linker peptide, or a functional
CC derivative or salt of (I). (I) is useful for reducing intracellular iron
CC absorption in patients having hereditary haemochromatosis, transfusions,
CC thalassemias, haemolytic anaemia or chronic infections, and for
CC delivering a therapeutic to cells that over-express transferrin receptor
CC (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC brain barrier. (I) is further useful for treating brain tumour. (I) is
CC also useful for treating oxidative stress disorders resulting in tissue
CC damage e.g. vascular diseases, inflammation, atherosclerosis, lung
CC injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful as a
CC platform for drug delivery of therapeutic use for cancer, autoimmune
CC diseases and inflammatory conditions. The monochain manifests specific
CC characteristics advantageous for drug delivery systems. It is a soluble,
CC stable and fully conformed protein. It binds specifically to transferrin
CC receptor (TfR) and therefore targets cells that over-express this
CC receptor. It is continuously internalised by the target cells, thus
CC enabling efficient drug delivery. It dissociates from the receptor in the
CC cells, minimising side effects. It negatively regulates iron absorption,
CC reducing growth of undesired cells and preventing lymphocyte activation.
CC It is not diluted in the blood as is transferrin. It should not induce an
CC immune response since it is a self non-polymeric protein and delivery of
CC drugs via monochain is expected to overcome drug-resistance since it is a
CC natural TfR-binding protein. The present sequence represents the coding
CC sequence of beta2m/HFE monochain
XX
SQ Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 U; 0 Other;
Query Match 100.0%; Score 601; DB 6; Length 1317;
Best Local Similarity 100.0%; Pred. No. 5.4e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGCAGTGCAGTGCAGTCTGAAAGGGTGGGATCATGTTCATCTTGAC 60
DB 580 CAGATGTGGCTGCAGTGCAGTGCAGTCTGAAAGGGTGGGATCATGTTCATCTTGAC 639
QY 61 TTCTGGACTATTATGGAATAATCACAACACAGCAAGGAGTCCACACCTCGAGTCTATC 120
DB 640 TTCTGGACTATTATGGAATAATCACAACACAGCAAGGAGTCCACACCTCGAGTCTATC 699
QY 121 TTGGGCTGTGAATGCAAGACACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
DB 700 TTGGGCTGTGAATGCAAGACACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 759
QY 181 GGGCAGGACCACTTGAATTTGCTCCCTGACACACATGGATTTGGAGAGCAGAACCCAGG 240
DB 760 GGGCAGGACCACTTGAATTTGCTCCCTGACACACATGGATTTGGAGAGCAGAACCCAGG 819
QY 241 GCCTGGCCCAACAAGCTGGAGTGGGAAGGACACAGATTCGGGCCAGGACGACAGGGCC 300
DB 820 GCCTGGCCCAACAAGCTGGAGTGGGAAGGACACAGATTCGGGCCAGGACGACAGGGCC 879
QY 301 TACCTGGAGAGGAGTGCCTGCACAGTGCAGCAGTGTGCTGGAGCTGGGAGAGGTGT 360
DB 880 TACCTGGAGAGGAGTGCCTGCACAGTGCAGCAGTGTGCTGGAGCTGGGAGAGGTGT 939
QY 361 TTGGACCAACAAGTGCCTCTTTGTGTGAAGGTGACATCATGTGACCTTTTCAGTGACC 420
DB 940 TTGGACCAACAAGTGCCTCTTTGTGTGAAGGTGACATCATGTGACCTTTTCAGTGACC 999
QY 421 ACTCTACGGTGTGCGGCTTGAACCTACTACCCCAAGACATCACCATGAGTGGCTGAAG 480
DB 1000 ACTCTACGGTGTGCGGCTTGAACCTACTACCCCAAGACATCACCATGAGTGGCTGAAG 1059
QY 481 GATAAGCAGCAATGGATGCCAAGGAGTTTGCAGACCTAAAGAGCTATTGCCCAATGGGAT 540
|||||

DB 1060 GATAGCAGCCCAATGGATGCCAAGGATTCGAACCTAAGACGCTATTGCCCAATGGGAT 1119
QY 541 GGGACCTACAGGGCTGGATAACCTTGTCTGTACCCCTGGGGAAAGACAGATATACG 600
|||||
DB 1120 GGGACCTACAGGGCTGGATAACCTTGTCTGTACCCCTGGGGAAAGACAGATATACG 1179
QY 601 T 601
DB 1180 T 1180
RESULT 2
ADG87336
ID ADG87336 standard; cDNA; 1439 BP.
XX AC ADG87336;
XX DT 11-MAR-2004 (first entry)
XX DE Hereditary haemochromatosis (HH) 24d7 mutant cDNA.
XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
XX KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
XX ss.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX CDS 222..1268
XX FT /*tag= a
XX FT /product= "Hereditary haemochromatosis 24d7 mutant
XX FT protein"
XX PN US2003148972-A1.
XX PD 07-AUG-2003.
XX PF 02-MAY-2002; 2002US-00138888.
XX PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
PR 04-APR-1997; 97US-00834497.
PR 04-FEB-2000; 2000US-00497957.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
PI Wolff RK;
XX WPI; 2003-897595/82.
DR P-PSDB; ADG87337.
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX Disclosure; SEQ ID NO 77; 122pp; English.
XX The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis 24d7 mutant
CC cDNA.
XX SQ Sequence 1439 BP; 345 A; 355 C; 407 G; 332 T; 0 U; 0 Other;
Query Match 100.0%; Score 601; DB 10; Length 1439;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
QY 61 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGAGTCCACACCTTCGACAGGTCATC 120
DB 525 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGAGTCCACACCTTCGACAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTTACGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTTACGGAAGTACGGGTATGAT 644
QY 181 GGGCAGGACCACTTGAATTTCTGCTGACACACTGGAATTGGAGAGCAGACAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTCTGCTGACACACTGGAATTGGAGAGCAGACAGAACCCAGG 704
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTCTGGGCCAGGCAAGAACAGGGCC 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTCTGGGCCAGGCAAGAACAGGGCC 764
QY 301 TACCTGGAGAGGACTGCTGCTGACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGTGT 360
DB 765 TACCTGGAGAGGACTGCTGCTGACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGTGT 824
QY 361 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 420
DB 825 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 884
QY 421 ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTAAAGACGATATCG 480
DB 885 ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTAAAGACGATATCG 944
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600
DB 1005 GGGACCTACAGGGCTGGATACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064
QY 601 T 601
DB 1065 T 1065

RESULT 3
ID ADG87270
AC ADG87270 standard; cDNA; 1439 BP.
AC ADG87270;
XX 11-MAR-2004 (first entry)
DE Hereditary haemochromatosis (HH) 24d2 mutant cDNA.
XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
KW 88.
XX Unidentified.
XX Key Location/Qualifiers
FT CDS 222..1268
FT /tag= a
FT /product= "Hereditary haemochromatosis 24d2 mutant
FT protein"
XX
PN US2003148972-A1.
XX
PD 07-AUG-2003.
XX
PF 02-MAY-2002; 2002US-00138888.

XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
PR 04-APR-1997; 97US-00834497.
PR 04-FEB-2000; 2000US-00497957.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Teuchihaashi Z;
PI Wolff RK;
XX
DR WPI; 2003-897595/82.
DR P-PSDB; ADG87265.
XX
XX New hereditary haemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX
PS Claim 1; SEQ ID NO 11; 122pp; English.
XX
CC The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis 24d2 mutant
CC cDNA.
XX
SQ Sequence 1439 BP; 346 A; 354 C; 408 G; 331 T; 0 U; 0 Other;
Query Match 100.0%; Score 601; DB 10; Length 1439;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
QY 61 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCTTCGACAGGTCATC 120
DB 525 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCTTCGACAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTTACGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTTACGGAAGTACGGGTATGAT 644
QY 181 GGGCAGGACCACTTGAATTTCTGCTGACACACTGGATTGGAGAGCAGACAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTCTGCTGACACACTGGATTGGAGAGCAGACAGAACCCAGG 704
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTCTGGGCCAGGCAAGAACAGGGCC 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTCTGGGCCAGGCAAGAACAGGGCC 764
QY 301 TACCTGGAGAGGACTGCTGCTGACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGTGT 360
DB 765 TACCTGGAGAGGACTGCTGCTGACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGTGT 824
QY 361 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 420
DB 825 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 884
QY 421 ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTAAAGACGATATCG 480
DB 885 ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTAAAGACGATATCG 944
QY 481 GATAGCAGCCCAATCGATGCCAAGAGTTCGAACCTTAAAGACGATATCGCCCAATGGGAT 540
DB 945 GATAGCAGCCCAATCGATGCCAAGAGTTCGAACCTTAAAGACGATATCGCCCAATGGGAT 1004
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600

1005 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 1064

Db 601 T 601
1065 T 1065

RESULT 4
ADG87268
ID ADG87268 standard; cDNA; 1439 Bp.

XX AC ADG87268;

XX 11-MAR-2004 (first entry)

XX Hereditary haemochromatosis (HH) wild-type cDNA.

XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; gene;
KW chromosome 6; ss.

XX OS Unidentified.

XX Key Location/Qualifiers

XX CDS 222..1268

XX FT /*tag= a

XX FT /product= "Hereditary haemochromatosis wild-type protein"

XX FT replace(408,G)

XX FT /*tag= b

XX FT /note= "24d2 mutation"

XX FT replace(414,T)

XX FT /*tag= c

XX FT /note= "24d7 mutation"

XX FT replace(1066,A)

XX FT /*tag= d

XX FT /note= "24d1 mutation"

XX US2003148972-A1.

XX 07-AUG-2003.

XX 02-MAY-2002; 2002US-00138888.

XX 04-APR-1996; 96US-00630912.

XX 16-APR-1996; 96US-00632673.

XX 23-MAY-1996; 96US-00652265.

XX 04-APR-1997; 97US-00834497.

XX 04-FEB-2000; 2000US-00497957.

XX (BIRA) BIO-RAD LAB INC.

XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihasi Z;

XX Wolff RK;

XX WPI; 2003-897595/82.

XX P-PSDB; ADG87261.

SQ Sequence 1439 BP; 346 A; 355 C; 407 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 601; DB 10; Length 1439;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGTTGGATCAGATCTTCACTCTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGTTGGATCAGATCTTCACTCTTGAC 524

QY 61 TTCTGGACTATTATGAAAAATCACAACCAAGCAGAGGAGTCCACACACCTGCAGGTCAATC 120
DB 525 TTCTGGACTATTATGAAAAATCACAACCAAGCAGAGGAGTCCACACACCTGCAGGTCAATC 584

QY 121 CTGGCTCTGAAATGCAAGAGACAAACAGTACCAGAGGCTACTGTGAAGTACGGGTATGAT 180
DB 585 CTGGCTCTGAAATGCAAGAGACAAACAGTACCAGAGGCTACTGTGAAGTATGATGAT 644

QY 181 GGGCAGGACCACTTGAATTTCTCCCTGACACACTGGAATTTGGAGAGCAGCAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTCTCCCTGACACACTGGAATTTGGAGAGCAGCAGAACCCAGG 704

QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGCAGAACAGGGCC 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGCAGAACAGGGCC 764

QY 301 TACCTGGAGAGGAGTGCCTGCAAGCTGCAGCAGATTTGCTGGAGCTGGGGAGAGGTGTT 360
DB 765 TACCTGGAGAGGAGTGCCTGCAAGCTGCAGCAGATTTGCTGGAGCTGGGGAGAGGTGTT 824

QY 361 TTGGACCAACAAGTGCCTTCTTGGTGAAGTGACACATCATGTGACCTCTTCACTGACC 420
DB 825 TTGGACCAACAAGTGCCTTCTTGGTGAAGTGACACATCATGTGACCTCTTCACTGACC 884

QY 421 ACTCTACCGTGTGGGGCTTGAATTAATCTACCCCAAGATCATCAGATGAAGTGGCTGAAG 480
DB 885 ACTCTACCGTGTGGGGCTTGAATTAATCTACCCCAAGATCATCAGATGAAGTGGCTGAAG 944

QY 481 GATAAGCAGCCAAATGGATGCCAAGAGTTCGAACCTAAAGAGTATTGCCAATGGGAT 540
DB 945 GATAAGCAGCCAAATGGATGCCAAGAGTTCGAACCTAAAGAGTATTGCCAATGGGAT 1004

QY 541 GGGACCTACAGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600
DB 1005 GGGACCTACAGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064

QY 601 T 601

DB 1065 T 1065

RESULT 5

ADG87271

ID ADG87271 standard; cDNA; 1439 Bp.

XX AC ADG87271;

XX 11-MAR-2004 (first entry)

XX Hereditary haemochromatosis (HH) mutant cDNA.

XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
KW ss.

XX OS Unidentified.

XX Key Location/Qualifiers

XX CDS 222..1268

XX FT /*tag= a

XX FT /product= "Hereditary haemochromatosis mutant protein
comprising 24d1 and 24d2 mutations."

XX

PN US2003148972-A1.
XX 07-AUG-2003.
XX 02-MAY-2002; 2002US-00138888.
XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
PR 04-APR-1997; 97US-00834497.
PR 04-FEB-2000; 2000US-00497957.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
PI Wolff RK;
XX WPI; 2003-897595/82.
DR P-PSDB; ADG87267.
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX Claim 1; SEQ ID NO 12; 122pp; English.
XX The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis mutant cDNA
CC comprising 24d1 and 24d2 mutations.
XX
SQ Sequence 1439 BP; 347 A; 354 C; 407 G; 331 T; 0 U; 0 Other;
Query Match 100.0%; Score 601; DB 10; Length 1439;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGATCACATGTTTCACTGTGTGAC 60
Db 465 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGATCACATGTTTCACTGTGTGAC 524
QY 61 TTCTGACTATTATGAAATCAACACAGGAGTCCACACCCCTGCAGGTCATC 120
Db 525 TTCTGACTATTATGAAATCAACACAGGAGTCCACACCCCTGCAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAGACACAGTACCAGGGGCTACTGGAAGTACGGGTATGAT 180
Db 585 CTGGGCTGTGAATGCAAGAGACACAGTACCAGGGGCTACTGGAAGTACGGGTATGAT 544
QY 181 GGCAGGACACCTTGAAATTCCTCTGACACACTGGATGAGAGACAGACAGCCAGG 240
Db 645 GGCAGGACACCTTGAAATTCCTCTGACACACTGGATGAGAGACAGACAGCCAGG 704
QY 241 GCTGGCCCAACCAAGCTGGAGTGGGAAGCACAAGATTGGGCCAGGACAGAGGCC 300
Db 705 GCTGGCCCAACCAAGCTGGAGTGGGAAGCACAAGATTGGGCCAGGACAGAGGCC 764
QY 301 TACCTGGAGGAGTGCCTCTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 360
Db 765 TACCTGGAGGAGTGCCTCTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 824
QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
QY 421 ACTCTACGGTGTGGGCGCTTGAAGTACTACCTACCTACCTACCTACCTACCTACCT 480
Db 885 ACTCTACGGTGTGGGCGCTTGAAGTACTACCTACCTACCTACCTACCTACCTACCT 944

QY 481 GATAAGCAGCCATGATGATGCAAGAGTTTGAACCTAAAGACCTATTGCCCAATGGGAT 540
Db 945 GATAAGCAGCCATGATGATGCAAGAGTTTGAACCTAAAGACCTATTGCCCAATGGGAT 1004
QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGACAGATATACG 600
Db 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGACAGATATACG 1064
QY 601 T 601
Db 1065 T 1065

RESULT 6

ADG87269
ID ADG87269 standard; cDNA; 1439 BP.
XX
AC ADG87269;
XX
DT 11-MAR-2004 (first entry)
XX
DE Hereditary haemochromatosis (HH) 24d1 mutant cDNA.
XX
KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
KW ss.
XX Unidentified.
XX
FH Key Location/Qualifiers
CDS 222..1268
FT /tag= a
FT /product= "Hereditary haemochromatosis 24d1 mutant
FT protein"
XX
PN US2003148972-A1.
XX
PD 07-AUG-2003.
XX
PF 02-MAY-2002; 2002US-00138888.
XX
PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
PR 04-APR-1997; 97US-00834497.
PR 04-FEB-2000; 2000US-00497957.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
PI Wolff RK;
XX
DR WPI; 2003-897595/82.
DR P-PSDB; ADG87263.
XX
PT New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX
XX Claim 1; SEQ ID NO 10; 122pp; English.
XX
CC The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis 24d1 mutant
CC cDNA.
XX
SQ Sequence 1439 BP; 347 A; 355 C; 406 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 601; DB 10; Length 1439;

Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTCAC 60
DB 465 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTCAC 524

QY 61 TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCTGCGAGTCAATC 120
DB 525 TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCTGCGAGTCAATC 584

QY 121 CTGGGCTGTAATCAAGACACACAGTACCGAGGGTCTCTGGAAGTACCGGTATGAT 180
DB 585 CTGGGCTGTAATCAAGACACACAGTACCGAGGGTCTCTGGAAGTACCGGTATGAT 644

QY 181 GGGCAGGACACCTTGAATTCCTCCCTGCACACACTGGATTGGAGAGCAGACAGCCAGG 240
DB 645 GGGCAGGACACCTTGAATTCCTCCCTGCACACACTGGATTGGAGAGCAGACAGCCAGG 704

QY 241 GCCTGGCCACCAAGCTGGAGTGGGAAGGCAAGATTTCGGGGCCAGGACAGAGGGCC 300
DB 705 GCCTGGCCACCAAGCTGGAGTGGGAAGGCAAGATTTCGGGGCCAGGACAGAGGGCC 764

QY 301 TACCTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGAGCTGGGAGAGGTGT 360
DB 765 TACCTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGAGCTGGGAGAGGTGT 824

QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
DB 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884

QY 421 ACTTACGTTGCTGGGCTTGAATCTACTACCCCGAAGATCACATGAGTGGCTGAAG 480
DB 885 ACTTACGTTGCTGGGCTTGAATCTACTACCCCGAAGATCACATGAGTGGCTGAAG 944

QY 481 GATAGCAGCAATGATGATCCAGAGTTCGAACCTTAAGAGCTATTGCCCAATGGGAT 540
DB 945 GATAGCAGCAATGATGATCCAGAGTTCGAACCTTAAGAGCTATTGCCCAATGGGAT 1004

QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGATATAGC 600
DB 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGATATAGC 1064

QY 601 T 601
DB 1065 T 1065

RESULT 7
AAT96691 ID AAT96691 standard; cDNA; 1440 BP.
XX AC AAT96691;
DT 14-APR-1998 (first entry)
XX DE Hereditary haemochromatosis gene cDNA clone.
XX KW Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy;
XX KW prenatal screening; human; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 222..1268
FT mutation /*tag= a
FT /*tag= g
FT /*note= "C to G substitution (24d2 mutation) results in
FT His to Asp substitution"
FT variation 414
FT /*tag= h
FT /*note= "A to T substitution (24d7 variant) results in Ser

FT mutation to Cys substitution"
FT 1066
FT /*tag= i
FT /*note= "G to A substitution (24d1 mutation associated
FT with HH), results in Cys to Tyr substitution"
XX
PN WO9738137-A1.
XX 16-OCT-1997.
XX 04-APR-1997; 97WO-US006254.
XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
XX (MERC-) MERCATOR GENETICS INC.
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
PI Wolff RK;
XX WPI; 1997-512743/47.
DR P-PSDB; AAW36499.
XX Hereditary haemochromatosis gene and variants - useful for diagnosis and
FT treatment of hereditary haemochromatosis disease.
XX Disclosure; Fig 4; 115pp; English.
XX This cDNA clone, designated cDNA24, is derived from human gene whose
CC mutated form is associated with hereditary haemochromatosis (HH). It was
CC obtained from a directionally cloned plasmid-based cDNA library following
CC identification of the HH locus in the HLA region of chromosome 6. A
CC single mutation (24d1) in the HH gene appears responsible for the
CC majority of HH disease. This comprises a G to A substitution that is
CC present in 86% of affected chromosomes and in 4% of unaffected
CC chromosomes. It results in a Cys to Tyr substitution in the encoded
CC protein (see AAW36499) at a critical disulphide bridge important for
CC secondary structure. The following are claimed: a 10825 bp genomic DNA
CC sequence (1) (see AAT96690), the 1437 bp cDNA sequence (1a) and their
CC 24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells;
CC a peptide product chosen from the HH gene product, its variants (24d1,
CC 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these;
CC an antibody produced using the peptide; a method to determine the
CC presence or absence of the common HH gene mutation; an animal model for
CC the HH disease; metal chelation agents, T-cell differentiation factors
CC and therapeutic agents for the mitigation of injury due to oxidative
CC process in vivo or mitigation of iron overload; a method for screening
CC potential therapeutic agents for activity in connection with HH disease;
CC an antisense oligonucleotide directed against a transcriptional product
CC of a nucleic acid sequence as above; and oligonucleotides or pairs of
CC oligonucleotides covering a range of nucleotides from (1), (1a) or their
CC variants, useful for detecting a polymorphism in the HH gene. The
CC invention also relates to methods for screening for HH homozygotes, to HH
CC diagnosis, prenatal screening and diagnosis, and therapies of HH disease,
CC including gene therapy, protein- and antibody-based therapeutics, and
CC small molecule therapeutics
XX
SQ Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 601; DB 2; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTCAC 60
DB 465 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTCAC 524

QY 61 TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCTGCGAGTCAATC 120
DB 525 TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCTGCGAGTCAATC 584

QY 121 CTGGGCTGTAATGGAATAACAAACACAGAGAGAGTCCACACCTGCGAGTCAATC 180

XX US6140305-A.
PN 31-OCT-2000.
XX 04-APR-1997; 97US-00834497.
XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX WPI; 2001-006341/01.
XX New hereditary hemochromatosis gene products or polypeptides, useful for
PT treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX Disclosure; Fig 4; 108pp; English.
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 601; DB 5; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGACGTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 60
DB 465 CAGATGTGGCTGACGTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 524
QY 61 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCCCTGCAGGTCATC 120
DB 525 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCCCTGCAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAGACACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGACACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644
QY 181 GGGCAGGACACCTTGAATTCGCCCTGACACTGGATTGGAGAGCAGACAGCCAGG 240
DB 645 GGGCAGGACACCTTGAATTCGCCCTGACACTGGATTGGAGAGCAGACAGCCAGG 704
QY 241 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTCCGGCCAGGCGAGAACCCAGG 300
DB 705 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTCCGGCCAGGCGAGAACCCAGG 764
QY 301 TACCTGGAGAGGAGTGCCTTCGACAGCTGCAGCAGTTCCTCGAGCTGGGGAGAGTGT 360
DB 765 TACCTGGAGAGGAGTGCCTTCGACAGCTGCAGCAGTTCCTCGAGCTGGGGAGAGTGT 824
QY 361 TTGGACCAACAAGTGCTCTTTGGTGAAGGTGACACATCATGTCACCTTCCTGAGTACC 420
DB 825 TTGGACCAACAAGTGCTCTTTGGTGAAGGTGACACATCATGTCACCTTCCTGAGTACC 884
QY 421 ACTCTACGCTGTGGGCTTTGAATCTACTACCCCAAGACATCACCAATGAAGTGGCTGAAG 480
DB 885 ACTCTACGCTGTGGGCTTTGAATCTACTACCCCAAGACATCACCAATGAAGTGGCTGAAG 944
QY 481 GATAAGCAGCCAAATGGATGCCAAGGAGTTGCAACCTTAAAGACGTATTGCCCCAATGGGAT 540
DB 945 GATAAGCAGCCAAATGGATGCCAAGGAGTTGCAACCTTAAAGACGTATTGCCCCAATGGGAT 1004

QY 541 GGGACCTACCGGGCTGGATAACCTTGCTGTACCCCTGGGAGAGCAGAGATATACG 600
DB 1005 GGGACCTACCGGGCTGGATAACCTTGCTGTACCCCTGGGAGAGCAGAGATATACG 1064
QY 601 T 601
DB 1065 T 1065
RESULT 10
AAC68431
ID AAC68431 standard; DNA; 1440 BP.
XX AAC68431;
AC AAC68431;
XX 21-FEB-2001 (first entry)
XX Human hereditary hemochromatosis 24d2 mutation cDNA.
XX HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX Homo sapiens.
XX OS
XX US6140305-A.
XX 31-OCT-2000.
XX 04-APR-1997; 97US-00834497.
PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX WPI; 2001-006341/01.
XX New hereditary hemochromatosis gene products or polypeptides, useful for
PT treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX Disclosure; Fig 4; 108pp; English.
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 601; DB 5; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.6e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGACGTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 60
DB 465 CAGATGTGGCTGACGTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 524
QY 61 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCCCTGCAGGTCATC 120
DB 525 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCCCTGCAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAGACACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGACACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644
QY 181 GGGCAGGACACCTTGAATTCGCCCTGACACTGGATTGGAGAGCAGACAGCCAGG 240

Db 645 GGCAGGACACCTTGAATTCGCTTGCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 704
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCACAAAGATTTCGGGCCAGGCAGAACAGGGCC 300
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCACAAAGATTTCGGGCCAGGCAGAACAGGGCC 764
QY 301 TACCTGGAGAGGAGCTGCCCTGACACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTT 360
Db 765 TACCTGGAGAGGAGCTGCCCTGACACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTT 824
QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
QY 421 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCAGAAACATCACCATTGAAGTGGCTGAAG 480
Db 885 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCAGAAACATCACCATTGAAGTGGCTGAAG 944
QY 481 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAAGACGTATTGGCCCAATGGGGAT 540
Db 945 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAAGACGTATTGGCCCAATGGGGAT 1004
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAGAGCAGATATACG 600
Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAGAGCAGATATACG 1064
QY 601 T 601
Db 1065 T 1065

RESULT 11

AAC68432

ID AAC68432 standard; DNA; 1440 BP.

AC AAC68432;

XX

XX 21-FEB-2001 (first entry)

XX Human hereditary hemochromatosis 24d1/2 mutation cDNA.

XX HH; hereditary hemochromatosis; chelation agent;

KW T-cell differentiation factor; iron overload; ss.

XX

XX Homo sapiens.

XX

XX US6140305-A.

XX

XX 31-OCT-2000.

XX

XX 04-APR-1997; 97US-00834497.

XX

XX 04-APR-1996; 96US-00630912.

XX

XX 16-APR-1996; 96US-00632673.

XX

XX 23-MAY-1996; 96US-00652265.

XX

XX (BIRA) BIO-RAD LAB INC.

XX

XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;

XX Feder JN;

XX

XX WPI; 2001-006341/01.

XX

XX New hereditary hemochromatosis gene products or polypeptides, useful for

XX

XX PT treating hereditary hemochromatosis in a patient, and as a metal

XX

XX chelation agent alleviating iron overload.

XX

XX Disclosure; Fig 4; 108pp; English.

XX

XX The present invention relates to hereditary hemochromatosis gene

XX

XX products. These proteins may be used to treat a patient diagnosed as

XX

XX having human hemochromatosis disease. It is also useful as a metal

CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX
SQ Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 601; DB 5; Length 1440;

Best Local Similarity 100.0%; Pred. No. 5.6e-160;

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGCTGCAGCTGAGTCTGAAGGGTGGGATCAGATGTTCTACTGTTCAC 60
Db 465 CAGATGTGCTGCAGCTGAGTCTGAAGGGTGGGATCAGATGTTCTACTGTTCAC 524
QY 61 TTCTGACCTATTATGAAATCAACACAGCAGCAAGAGTCCACACCTTCAGAGTCATC 120
Db 525 TTCTGACCTATTATGAAATCAACACAGCAGCAAGAGTCCACACCTTCAGAGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTTCTGGAAGTACGGGTATGAT 180
Db 585 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTTCTGGAAGTACGGGTATGAT 644
QY 181 GGGCAGGACCACTTGAATTTGCTCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240
Db 645 GGGCAGGACCACTTGAATTTGCTCCTGACACACTGGATTGGAGAGCAGAACCCAGG 704
QY 241 GCTGGCCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACGGCC 300
Db 705 GCTGGCCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACGGCC 764
QY 301 TACCTGGAGAGGAGCTGCCCTGACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTT 360
Db 765 TACCTGGAGAGGAGCTGCCCTGACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTT 824
QY 361 TTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 825 TTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
QY 421 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCAGAAACATCACCATTGAAGTGGCTGAAG 480
Db 885 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCAGAAACATCACCATTGAAGTGGCTGAAG 944
QY 481 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAAGACGTATTGGCCCAATGGGGAT 540
Db 945 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAAGACGTATTGGCCCAATGGGGAT 1004
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAGAGCAGATATACG 600
Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAGAGCAGATATACG 1064
QY 601 T 601
Db 1065 T 1065

RESULT 12

AAA96769

ID AAA96769 standard; cDNA; 2506 BP.

XX

XX AAA96769;

XX

XX 19-FEB-2001 (first entry)

XX

XX cDNA sequence encoding a histocompatibility iron loading (HFE) protein.

XX

XX Human; histocompatibility iron loading protein; HFE protein;

XX major histocompatibility complex; non-classical class I gene;

XX chromosome 6p; iron disorder; haemochromatosis; ss.

XX

XX Homo sapiens.

XX

XX Key

XX Location/Qualifiers

XX 1..1044

XX CDS

FT		/tag= a	
FT		/product= "histocompatibility iron loading (HFE) protein"	
FT	sig_peptide	1. .66	
FT		/tag= b	
FT	mutation	187	
FT		/tag= c	
FT		/note= "if this base is mutated to G, then the protein contains the mutation H63D"	
FT	mutation	193	
FT		/tag= d	
FT		/note= "if this base is mutated to T, then the protein contains the mutation S65C"	
FT	mutation	277	
FT		/tag= e	
FT		/note= "if this base is mutated to C, then the protein contains the mutation G93R"	
FT	mutation	314	
FT		/tag= f	
FT		/note= "if this base is mutated to C, then the protein contains the mutation I105T, which is associated with an iron overload disorder"	
XX			
XX			
PN	WO200059515-A1.		
XX			
XX	05-OCT-2000.		
XX			
XX	24-MAR-2000; 2000WO-US007982.		
XX			
PR	26-MAR-1999; 99US-00277457.		
XX			
XX	(BILL-) BILLUPS-ROTHENBERG INC.		
XX			
PI	Rothenberg BE, Sawada-Hirai R, Barton JC;		
XX			
DR	WPI; 2000-647244/62.		
DR	P-PSDB; AAB19149.		
XX			
PT	Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid.		
PT			
PT			
XX	Disclosure; Page 2-3; 55pp; English.		
XX			
CC	The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A36769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop it		
XX			
SQ	Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 U; 0 Other;		
Query Match 100.0%; Score 601; DB 3; Length 2506;			
Best Local Similarity 100.0%; Pred. No. 6.9e-160;			
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CAGATGTGCTGCAGCTGAGTCAGAGTCTGAAGGGTGGGATCACATGTTCACTGTTGAC	60
Db	244	CAGATGTGCTGCAGCTGAGTCAGAGTCTGAAGGGTGGGATCACATGTTCACTGTTGAC	303
QY	61	TTCGTGACTATTATGGAAATCACAAACACAGCAGGAGTCCCAACCCCTGCAGGTCACT	120
Db	304	TTCGTGACTATTATGGAAATCACAAACACAGCAGGAGTCCCAACCCCTGCAGGTCACT	363
QY	121	CTGGGCTGTGAATGCAAGAACAACAGTACCCGAGGGCTACTCGAAGTACGGGTATGAT	180
Db	364	CTGGGCTGTGAATGCAAGAACAACAGTACCCGAGGGCTACTCGAAGTACGGGTATGAT	423

Db 525 TTCTGGACTATTATGAAATCACAACCAACAGAGGTCCACACCTCGAGGTATC 584
Qy 121 CTGGGCTGTGAATCAAGAAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
Db 585 CTGGGCTGTGAATCAAGAAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644
Qy 181 GGGCAGGACACCTTGAATTCGCTTGACACACTGGATTGGAGAGCAGACAACCCAGG 240
Db 645 GGGCAGGACACCTTGAATTCGCTTGACACACTGGATTGGAGAGCAGACAACCCAGG 704
Qy 241 GCTTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTGCGGCGCAGGCAAGACAGGGCC 300
Db 705 GCTTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTGCGGCGCAGGCAAGACAGGGCC 764
Qy 301 TACCTGGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGTGT 360
Db 765 TACCTGGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGTGT 824
Qy 361 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 825 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
Qy 421 ACTCTACGCTGTCGCGCTTGAACCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 480
Db 885 ACTCTACGCTGTCGCGCTTGAACCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 944
Qy 481 GATAAGCAGCAATGGATGCCAAGAGTTGCAACCTTAAAGACGTATTGCCCAATGGGAT 540
Db 945 GATAAGCAGCAATGGATGCCAAGAGTTGCAACCTTAAAGACGTATTGCCCAATGGGAT 1004
Qy 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTATACCCCTGGGGAAGAGAGATATACG 600
Db 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTATACCCCTGGGGAAGAGAGATATACG 1064
Qy 601 T 601
Db 1065 T 1065
RESULT 15
ID ADP65373
AC ADP65373 standard; DNA; 2727 BP.
XX ADP65373;
XX 12-AUG-2004 (first entry)
XX Human haemochromatosis protein (HLA-H) mRNA, complete cds DNA.
XX autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; ds; human.
XX Homo sapiens.
XX WO2003072827-A1.
XX 04-SEP-2003.
XX 31-OCT-2002; 2002WO-US035433.
XX 31-OCT-2001; 2001US-0336220P.
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX Hirsch R, Thorton SL;
PI WPI: 2003-712740/67.
DR GENBANK; U60319.

XX Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX Disclosure; Page; 56pp; English.
XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This polynucleotide
CC represents a DNA sequence relating to the genes used in the analysis and
CC treatment of autoimmune diseases or arthritides. Note: This sequence is
CC not shown in the specification. It has been supplied in an electronic
CC format from WIPO.
XX SQ Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 U; 0 Other;
Query Match 100.0%; Score 601; DB 11; Length 2727;
Best Local Similarity 100.0%; Pred. No. 7.1e-160;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGATGTGGCTGCGAGCTGAGTCAGAGTCTGAAAGGGTGGGATCATCATGTTTCATCTTGAC 60
Db 465 CAGATGTGGCTGCGAGCTGAGTCAGAGTCTGAAAGGGTGGGATCATCATGTTTCATCTTGAC 524
Qy 61 TTCTGGACTATTATGGAATAATCAACCAAGCAAGAGAGTCCCAACCCCTGCGAGTCTATC 120
Db 525 TTCTGGACTATTATGGAATAATCAACCAAGCAAGAGAGTCCCAACCCCTGCGAGTCTATC 584
Qy 121 CTGGGCTGTGAATGCAAGAGACACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
Db 585 CTGGGCTGTGAATGCAAGAGACACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644
Qy 181 GGGCAGGACACCTTGAATTCGCTTGACACACTGGATTGGAGAGCAGACAACCCAGG 240
Db 645 GGGCAGGACACCTTGAATTCGCTTGACACACTGGATTGGAGAGCAGACAACCCAGG 704
Qy 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTTCGGGCGCAGGCAAGACAGGGCC 300
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTTCGGGCGCAGGCAAGACAGGGCC 764
Qy 301 TACCTGGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTTCGCTGGAGAGAGTGT 360
Db 765 TACCTGGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTTCGCTGGAGAGAGTGT 824
Qy 361 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 825 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
Qy 421 ACTCTACGCTGTCGCGCTTGAACCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 480
Db 885 ACTCTACGCTGTCGCGCTTGAACCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 944

Qy	481	GATAAGCAGCCAATGGATGCCAAGGAGTTGAACTAAAGACGTATTGCCCAATGGGAT	540
Db	945	GATAAGCAGCCAATGGATGCCAAGGAGTTGAACTAAAGACGTATTGCCCAATGGGAT	1004
Qy	541	GGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCTGGGAAGACAGAGATATACG	600
Db	1005	GGGACCTACCAGGCTGGATAACCTTGGCTGTACCCCTGGGAAGACAGAGATATACG	1064
Qy	601	T	601
Db	1065	T	1065

Search completed: June 22, 2005, 11:13:46
Job time : 309.314 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 09:06:57 ; Search time 1892.7 Seconds
(without alignments)

12086.738 Million cell updates/sec

Title: US-09-497-957-9_COPY_465_1065

Perfect score: 601

Sequence: 1 CAGATGTGCTGCAGCTGAG.....GGAAGACGAGATATACCT 601

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	565	94.0	819	4	BG747345
2	491.8	81.8	570	2	BE272926
3	397	64.4	729	6	CB529554
4	359	59.7	1719	3	AK088896
5	359	59.7	1723	3	AK009581
6	350	58.2	603	7	CN264281
7	324.2	53.9	820	5	BP434195
8	282	46.9	560	1	AU279987
9	261.8	43.6	535	6	CB162561
10	260	43.3	544	4	BM751283
11	257.2	42.8	825	5	BU746849
12	251.4	41.8	457	1	AI850020
13	248.4	41.3	455	2	BE995172
14	244.6	40.7	542	6	CA569584
15	230	38.3	384	2	BF983952
16	229	38.1	871	5	BU746860
17	219	36.4	799	7	CK366555
18	214.6	35.7	546	2	BE809138
19	199.6	33.2	481	5	BQ561639
20	178	29.6	668	4	BM723847
21	174	29.0	394	2	BF464345
22	160.4	26.7	645	1	AU296357
23	151.8	25.3	289	7	H33644
24	149.6	24.9	668	6	BY745026

ALIGNMENTS

RESULT 1	25	146	24.3	531	8	AQ703007	AQ703007 HS 5443 B
LOCUS	26	138.4	23.0	444	8	AZ025590	AZ025590 RPTC-23-3
DEFINITION	27	136.6	22.7	492	9	CG578705	CG578705 OST216218
ACCESSION	28	131.6	21.9	489	2	BE994943	BE994943 UI-M-CG0P
VERSION	29	130	21.6	807	7	CO571571	CO571571 AGENCOURT
KEYWORDS	30	129.6	21.6	737	5	BM919242	BM919242 AGENCOURT
SOURCE	31	129.6	21.6	1041	5	BM919242	BM919242 AGENCOURT
ORGANISM	32	129.4	21.5	579	5	BP333106	BP333106 AGENCOURT
REFERENCE	33	129.2	21.5	550	4	BI339179	BI339179 364041 MA
AUTHORS	34	128.8	21.4	1005	6	BY705256	BY705256 BY705256
TITLE	35	128.8	21.4	1021	5	BM920008	BM920008 AGENCOURT
JOURNAL	36	128.8	21.4	1298	3	AK005051	AK005051 Mus muscu
COMMENT	37	127.2	21.2	656	7	CK429585	CK429585 OJ38e12.Y
	38	127	21.1	979	7	CO579967	CO579967 ILLUMIGEN
	39	125.6	20.9	526	2	BF192528	BF192528 243759 MA
	40	125.6	20.9	582	1	AV691580	AV691580 AV691580
	41	124.8	20.8	521	2	BE808803	BE808803 214082 MA
	42	124.8	20.8	536	8	AZ074871	AZ074871 RPTC-23-4
	43	124.6	20.7	464	1	AA217236	AA217236 mu89b05.F
	44	124.6	20.7	763	7	CO568645	CO568645 AGENCOURT
	45	124.6	20.7	953	7	CO583074	CO583074 ILLUMIGEN

819 bp mRNA linear EST 15-MAY-2001
602704818F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4857941 5',
mRNA sequence.
BG747345
BG747345
BG747345.1 GI:14057998
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1711 row: d column: 06
High quality sequence stop: 792.
Location/Qualifiers
1. 819
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4857941"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Lib=NIH MGC 15"
/note="Organ: colon; Vector: pOTB7; Site: 1; XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

Query Match 94.0%; Score 565; DB 4; Length 819;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 729)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjh-m-12-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DriOB (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGG"

ORIGIN

Query Match 64.4%; Score 387; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 5.2e-95;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 215 TGGATTGGAGCAGCAGAACCCAGGGCTGGCCACCAAGCTGGAGTGGGAAGGCACA 274
DB 729 TGGATTGGAGCAGCAGAACCCAGGGCTGGCCACCAAGCTGGAGTGGGAAGGCACA 670
QY 275 AGATTCCGGCCAGCAGACAGGGCTTACTCTGAGAGGAGTCTCCCTGACACAGCTGCAGC 334
DB 669 AGATTCCGGCCAGCAGACAGGGCTTACTCTGAGAGGAGTCTCCCTGACACAGCTGCAGC 610
QY 335 AGTTGCTGGAGCTGGGGAGAGGTGTTTGGACCAACAAGTCCCTCTTTGGTGAAGGTGA 394
DB 609 AGTTGCTGGAGCTGGGGAGAGGTGTTTGGACCAACAAGTCCCTCTTTGGTGAAGGTGA 550
QY 395 CACATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGGGGCTTTGAACCTACTACCCCC 454
DB 549 CACATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGGGGCTTTGAACCTACTACCCCC 490

QY 455 AGAACATCACCATTGAAGTGGCTGAAGATAAGCAGCAATGAGTCCCAAGGAGTTTCAAC 514
DB 489 AGAACATCACCATTGAAGTGGCTGAAGATAAGCAGCAATGAGTCCCAAGGAGTTTCAAC 430
QY 515 CTAAGAAGCTATTGGCCCAATGGGATGGGACCTACCAAGGGCTGGATAACCTTGGCTGTAC 574
DB 429 CTAAGAAGCTATTGGCCCAATGGGATGGGACCTACCAAGGGCTGGATAACCTTGGCTGTAC 370
QY 575 CCCTGGGAGAGCAGCAGATATACCT 601
DB 369 CCCTGGGAGAGCAGCAGATATACCT 343
RESULT 4
AK088986 1719 bp mRNA linear HTC 03-APR-2004
LOCUS
DEFINITION Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430034J19 product:hemochromatosis, full insert sequence.
ACCESSION AK088986
VERSION AK088986.1 GI:26354115
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE 10349636
PUBMED
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
TITLE Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20493374
MEDLINE 11042159
PUBMED
REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
AUTHORS RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
TITLE Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL 20530913
MEDLINE 11076861
PUBMED
REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
AUTHORS Functional annotation of a full-length mouse cDNA collection
TITLE Nature 409, 685-690 (2001)
JOURNAL
MEDLINE
PUBMED
REFERENCE 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
AUTHORS Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
TITLE Nature 420, 563-573 (2002)
JOURNAL 6 (bases 1 to 1719)
MEDLINE
PUBMED
REFERENCE 6 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216).

cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

polyA signal

polyA site

avtarpant = 3000 /

59.7%: 500

ORIGIN

Query Match 59.7%; Score 359; DB 3; Length 1719;
Best Local Similarity 75.4%; Pred. NO. 3.3e-87;
Matches 471; Conservative 0; Mismatches 130; Indels 24; Gaps 1;

Qy	1	CAGATGTGGCTGCAGCTCAGTCTGAGCTCTGAAGGGTGGGATCACATGTTCACTGTTGAC	60
Db	349	CAGCTGTGGCTGCATCTTGAGTCTGAGAGCTGAAAGGGTGGGACTACATGTTCATAGTAGAC	408

Qy 97 GAGTCCCAACCCCTGCAGGTATCCTCGGCTGTGAATGCAAGAACAACAGTACCAG 156
| | | | |
Db 469 GAGTCCCACATCTGCAAGTGTCCTAGCTGTGAGGTGCTAAGAACAACAGTACCAGC 528
| | | | |

157	QY	GGCTACTGGAAGTACGGGTATGATGGCAGGACCACTTGAATTTCTGCCCTGCACACTG	216
529	Db	GGCTTCTGGAGATATGGTTATGACGGGCAAGATCACCTTGAATTTCTGCCCCAGACACTA	588
217	QY	GATTTGGAGAGCAGCAAGACCCACAGGGCTCGGCCACCAAGCTGGAGTGGGAAAGGCACAAG	276
589	Db	AACCTGGAGCGCAGCCGAGCCAGGGGCTTGGGCCACCAAGGTGGAATGGGACGAGCACAAG	648
277	QY	ATTCTGGGCCAGGCAGAACACAGGGCCTTACTTGGAGAGGGACTGCCCTCTGCAAGCTTGCAGCAG	336
649	Db	ATCCGTGCCAAAACAGAAACAGGGACTACTTGGAGAAGGACTGCCCCGACGAGCTGAAAACGG	708
337	QY	TTTCTCGAGCTGGGAGAGAGTGTTTTGGACCAACAAAGTGCCTCTTTGGTGAAGGTGACA	396
709	Db	CTCTCGAGCTGGGAGAGGCGTCTTGGGACACAAAGTGCCTACTTTGGTGAAGGTGACT	768
397	QY	CATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGGGCGCTTGAACACTACTACCCCCAG	456
769	Db	CGCCACTGGGCTCTACGGGGACCTCTCTAAGGTGTCAAGCTCTGGACTTCTTCTCCCCAG	828
457	QY	AACATCACCATGAAGTGGCTGAAGGATVAGCAGCCAAATGGATGCCAAGGAGTTGGAACCT	516
829	Db	AACATCACTATGAGTGGTTTGAAGGACAACCAACCACTGGATGCCAAGATGTCAACCCC	888
517	QY	AAAGACGATTTTGCCCAATGGGGATGGACCTACACGGCTTGGATAACTTTGGCTGTACCC	576
889	Db	GAGAAAGTCTGCTCTAACGGAGATGAGACCTCATCAGGCTGGCTGACGTTGGCAGTGCC	948
577	QY	CCTGGGGAAGACAGAGATATACGT	601
949	Db	CCTGGGGACGAGCAAGGTTCACT	973

RESULT 5

AK009581

LOCUS	DEFINITION
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LOCUS	AK009581	1723 bp	linear	HTC 03-APR-2000
DEFINITION	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04 product:hemochromatosis, full insert sequence.			

ACCESSION

VERSION

KEYWORDS
SOURCE

ORGANISMI

REFERENCE

REFERENCES

TITLE

JOURNAL
MEDICINEMEDLINE
PUBMED

REFERENCE

AUTHORS

TITLE

.....

JOURNAL
MEDICAL TIMEMEDLINE
PUBMED

REFERENCE

AUTHORS

TITLE

1000

JOURNAL
MEDICINEMEDLINE
PUBMED

Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 603 Std Error: 0.00.

FEATURES

Location/Qualifiers
1. .603
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryonic bodies
derived from H1, H7 and H9 cells"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowth derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 58.2%; Score 350; DB 7; Length 603;
Best Local Similarity 100.0%; Pred. No. 7.1e-85;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGTGGGATCAGATGTTCACTGTTGAC 60
Db 254 CAGATGTGGCTGAGCTGAGTCTGAAAGGTGGGATCAGATGTTCACTGTTGAC 313
QY 61 TTCTGGACTATTATGAAATCACAACACAGAGGAGTCCACACCTGCGAGTTCATC 120
Db 314 TTCTGGACTATTATGAAATCACAACACAGAGGAGTCCACACCTGCGAGTTCATC 373
QY 121 CTGGGCTGTGAATCAAGAAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
Db 374 CTGGGCTGTGAATCAAGAAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 433
QY 181 GGGCAGGACACCTTGAATTCCTGACACACTGGATGGAGAGCAGACAGCCAGG 240
Db 434 GGGCAGGACACCTTGAATTCCTGACACACTGGATGGAGAGCAGACAGCCAGG 493
QY 241 GCTGCCCCCAGAGCTGAGTGGGAAAGGCAAGATTCGGGCCAGGAGAGGGCC 300
Db 494 GCTGCCCCCAGAGCTGAGTGGGAAAGGCAAGATTCGGGCCAGGAGAGGGCC 553
QY 301 TACTGGAGAGGAGCTGCCCTGACAGCTGCAGCAGTTCCTGAGAGTGGG 350
Db 554 TACTGGAGAGGAGCTGCCCTGACAGCTGCAGCAGTTCCTGAGAGTGGG 603

RESULT 7

BP434195 820 bp mRNA linear EST 30-DEC-2003
LOCUS BP434195 full-length enriched swine cDNA library, adult lung Sus
DEFINITION BP434195 scrofa cDNA clone LNC010092B03 5', mRNA sequence.
ACCESSION BP434195
VERSION BP434195.1 GI:40424262
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
TITLE 1 (bases 1 to 820)
JOURNAL Unishii, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamasima, N., and Awata, T.
COMMENT PEDE (Pig Est Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Unishii
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627

Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES

Location/Qualifiers
1. .820
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="LNC010092B03"
/tissue_type="lung"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
lung"

ORIGIN

Query Match 53.9%; Score 324.2; DB 5; Length 820;
Best Local Similarity 81.3%; Pred. No. 9.4e-78;
Matches 399; Conservative 0; Mismatches 68; Indels 24; Gaps 1;
QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGTGGGATCAGATGTTCACTGTTGAC 60
Db 330 CAACTGTGGCTGAGCTAAGCCAGAGCCTGAAAGGTGGGATCAGATGTTCACTGTTGAC 389
QY 61 TTCTGGACTATTATGAAATCACAACACAGCAGCAG----- 96
Db 390 TTCTGGACTATTATGAAATCACAACACAGCAGCAGTACCAAGTGGGAGTGTGCCA 449
QY 97 GAGTCCCCACACCTGCGAGTCTCTGGGCTGTGAAATGCAAGAGACAAACAGTACCGAG 156
Db 450 GAGTCCCCACACCTGCGAGTCTCTGGGCTGTGAAATGCAAGAGCAGCAGCAGCAG 509
QY 157 GCGTCTGGAAGTACGGGTATGATGGGAGGAGCAGCCTTGAATTCGCCCTGACACACTG 216
Db 510 GCGTCTGGAAGTATGGGTATGATGGGAGGAGCAGCCTTGAATTCGCCCTGAGAGCTG 569
QY 217 GATTCGAGAGCAGAGACCCAGAGGCTGGGCCACCAAGCTGAGTGGGAAAGGCAAG 276
Db 570 GACTGGGGGGCGGAGAGCCAGAGGCTGGGCCACCAAGCTGAGTGGGAAAGTCAAG 629
QY 277 ATTCGGGGCGGAGAGAGGCTTACCTGGAGAGGAGTCCCTGCAAGCTGCAGCTGCAGCAG 336
Db 630 ATTCGGGGCGGAGAGAGGCTTACCTGGAGAGGAGTCCCTGCGGAGCAGCTGCGGGCG 689
QY 337 TTGCTGGAGCTGGGAGAGGTTTGGACCAAGTGGCTCCTTGGTGAAGTGACA 396
Db 690 TTGCTGGAGCTGGGAGAGGTTTGGACCAAGTGGCTCCTTGGTGAAGTGACT 749
QY 397 CATCATGTGACCTCTTCAGTGACCACTCTACGGTGTGGGGCTTGAACCTACTACCCCCAG 456
Db 750 CATCATGTGACCTCTTCAGTGACCACTCTACGGTGTGGGGCTTGAACCTACTACCCCCAG 809
QY 457 AACATCACCAT 467
Db 810 AACATCACCAT 820

RESULT 8

AU279987 560 bp mRNA linear EST 31-JUL-2003
LOCUS AU279987 CHONS2 Homo sapiens cDNA clone CHONS2002538 5', mRNA
DEFINITION AU279987 sequence.
ACCESSION AU279987
VERSION AU279987.1 GI:28299214
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 560)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Inabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isogai, T., Hata, J., Tomoya, Y., and Umezawa, A.
 COMMENT Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis
 JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)
 MEDLINE 22760698
 PUBMED 12878157
 CONTACT: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project, Sugiyama, T.; Wakamatsu, A.; Irie, R.; Umezawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.; Isono, Y.; Saito, K.; Nakamura, Y.; Masuho, Y.; Nagai, K.; Isogai, T.
 HRI human cDNA project; cDNA library construction & 5'-end one pass sequencing; Helix Research Institute.
 location/Qualifiers

FEATURES

source
 1..560
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CHONS2002538"
 /cell_type="chondrocytes"
 /clone_lib="CHONS2"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 46.9%; Score 282; DB 1; Length 560;
 Best Local Similarity 100.0%; Pred. No. 3.3e-66;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
 DB 279 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 338
 QY 61 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTCA 120
 DB 339 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTCA 398
 QY 121 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180
 DB 399 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 458
 QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAGCCAGG 240
 DB 459 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAGCCAGG 518
 QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTGG 282
 DB 519 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTGG 560

RESULT 9
 CB162561
 LOCUS K-EST0223175 L17N670205n1 Homo sapiens cDNA clone EST 30-JAN-2003
 DEFINITION L17N670205n1-27-D07 5', mRNA sequence.
 ACCESSION CB162561
 VERSION CB162561.1 GI:28148687
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 535)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

TITLE

JOURNAL
 COMMENT

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genomic Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 27 row: D column: 07
 High quality sequence stop: 535.
 Location/Qualifiers

FEATURES

source
 1..535
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L17N670205n1-27-D07"
 /sex="F"
 /lab_host="Top10P"
 /clone_lib="L17N670205n1"
 /note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."
 location/Qualifiers

ORIGIN

Query Match 43.6%; Score 261.8; DB 6; Length 535;
 Best Local Similarity 99.2%; Pred. No. 1.1e-60;
 Matches 263; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
 DB 271 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 330
 QY 61 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTCA 120
 DB 331 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTCA 390
 QY 121 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180
 DB 391 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 450
 QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAGCCAGG 240
 DB 451 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAGCCAGG 510
 QY 241 GCCTGGCCCAACCAAGCTGGAGTGGG 265
 DB 511 GCCTGGCCCAACCAAGCTGGAGTGGG 535

RESULT 10

BM751283
 LOCUS K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5', mRNA sequence.
 DEFINITION BM751283
 ACCESSION BM751283.1 GI:19080901
 VERSION BM751283.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 544)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)

COMMENT

Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.

FEATURES

Location/Qualifiers
1..544
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S9SNU601-12-G03"
/sex="M"
/tissue_type="Aescites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Top10F"
/clone_lib="S9SNU601"
/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Source

Query Match 43.3%; Score 260; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 CAGATGTGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
|||
Db 285 CAGATGTGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 344
|||
QY 61 TTCTGGACTATTATGAAATACACACCAGCAGCAGGAGTCCACACCCCTGCAGGTCATC 120
|||
Db 345 TTCTGGACTATTATGAAATACACACCAGCAGCAGGAGTCCACACCCCTGCAGGTCATC 404
|||
QY 121 CTGGGCTGTGAATGCAAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
|||
Db 405 CTGGGCTGTGAATGCAAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 464
|||
QY 181 GGGCAGGACACCTTGAATTCGCCCTGCACACTGGATTGGAGCAGCAGACCCAGG 240
|||
Db 465 GGGCAGGACACCTTGAATTCGCCCTGCACACTGGATTGGAGCAGCAGACCCAGG 524
|||
QY 241 GCTGGCCCCACCAAGCTGGA 260
|||
Db 525 GCTGGCCCCACCAAGCTGGA 544
|||

RESULT 11

BU746849 825 bp mRNA linear EST 10-OCT-2002
LOCUS CH3#007_D04T7 Canine heart normalized cDNA library in pBluescript
DEFINITION Canis familiaris cDNA clone CH3#007_D04 5', mRNA sequence.
ACCESSION BU746849
VERSION BU746849.1 GI:23697227
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE

AUTHORS Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A. L.
TITLE Expressed sequence tags from Canine heart
JOURNAL Unpublished (2003)
COMMENT Contact: George A. L.
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1739 Std Error: 0.00
Seq primer: 77: TAATACGACTCACTATAGGG
High quality sequence start: 41
High quality sequence stop: 561.

FEATURES

Source

1..825
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH3#007_D04"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"
/clone_lib="Canine heart normalized cDNA Library in pBluescript"
/note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"

ORIGIN

Query Match 42.8%; Score 257.2; DB 5; Length 825;
Best Local Similarity 79.9%; Pred. No. 2.3e-59;
Matches 326; Conservative 0; Mismatches 58; Indels 24; Gaps 1;

QY 1 CAGATGTGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
|||
Db 115 CAGCTGTGGTACAGCTGAGTCAGAGCTGAAGGGTGGGATCACATGTTCACTGTCGAC 174
|||
QY 61 TTCTGGACTATTATGAAATACACACCAGCAGCAG----- 96
|||
Db 175 TTCTGGACTATTATGAAATACACACCAGCAGCAGTAAAGCTCGGGGTATCGTCT 234
|||
QY 97 GAGTCCCAACCCCTCAGGTCATCTCGGCTGTGAATGCAAGACACACAGTACCGAG 156
|||
Db 235 GAGTCCCAACCTCTCAAGTGTATCTGGGCTGTGAGGTGCAAGAGCAACACACCA 294
|||
QY 157 GCCTACTGGAAGTACGGGTATGATGGCAGGACCACTTTGAATTTCTGCCCTGCACACTG 216
|||
Db 295 GGGTTCTGGAAGTATGGGTATGACCGACAGAACCACTTGGAAATTCGCCCTGAGAGCTG 354
|||
QY 217 GATTGGAGAGCAGAGAACCCAGGGCTTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAG 276
|||
Db 355 GATTGGAGAGCAGCGAGGCCCAAGGCCACCAAGCTGGAGTGGGAAAGTGAACAAG 414
|||
QY 277 ATTTCGGCCAGGCAGAACAGGGCTTACCTGGAGAGGAGTCCCTGCACAGCTGCGAGCAG 336
|||
Db 415 ATTTCGGCCAAACAGAACAGGGCTTACCTGCAGAGGGGATTGTCTGAGCAGCTGCGGCGAG 474
|||
QY 337 TTCTGGAGCTGGCAGAGGTGTTTTGGACCAACAAAGTGCCTCTCTTTG 384
|||
Db 475 CTGCTGGAGCTGGGAGAGGGGTTCTAGACCGCGAAGAGGCCCGCATG 522
|||

RESULT 12

AI850020 457 bp mRNA linear EST 15-JUL-1999
LOCUS AI850020

DEFINITION UI-M-BGO-aib-g-10-0-UI.s1 NIH BMAP MSC Mus musculus cDNA clone
 UI-M-BGO-aib-g-10-0-UI 3', mRNA sequence.
 ACCESSION AI850020
 VERSION AI850020.1 GI:5493926
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 457)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mEST@mail.nih.gov
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 The following repetitive elements were found in this cDNA sequence:
 3-30, >(CAG)n#Simple repeat
 Seq primer: M13 Forward
 POLYA=No.

FEATURES
 source
 1..457
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BGO-aib-g-10-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DHI08 (Life Technologies)"
 /clone_lib="NIH BMAP MSC"
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH BMAP MSC library is a non-normalized library
 constructed from mouse spinal cord. The tag is a string
 of 5 nucleotides present between the Not I site and the
 oligo-dT track. The library was constructed as described
 by Bonaldo, Lennon and Soares, Genome Research 6:
 791-806, 1996. Tissue provided by Ms. Annie Novakovich,
 Zivic-Miller Laboratories.
 TAG_TISSUE=spinal-cord
 TAG_LIB=NIH BMAP MSC
 TAG_SEQ=TCGAA"

ORIGIN
 Query Match 41.8%; Score 251.4; DB 1; Length 457;
 Best Local Similarity 79.8%; Pred. No. 7.7e-58;
 Matches 297; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 97 GAGTCCACACCTGCAGGTCATCTCTGGGCTGTGAATGCAAGACAAACAGTACCGAG 156
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 DB 85 GAGTCCACATCTCTGCAGGTGCTTCTAGGCTGTGAGTGCATGATGACACAGTACCAGC 144
 |||||
 QY 157 GGCTACTGGAAGTACGGGTATGATGGCAGGACCACTTGAATTCCTCCCTGCACACTG 216
 |||||
 DB 145 GGCTTCTGGAGATATGTTATGACGGCGCAAGATCACCTGGAATTCCTGCCCAAGACTA 204
 |||||
 QY 217 GATTGAGAGCAGCAGACCCAGGCTGATGATGGCAGGACCACTTGAATTCCTCCCTGCACACTG 276
 |||||
 DB 205 AACTGAGGCGACCGACGAGCGGCTGGGCCACCAAGTGTGAATGGGACGACGACAAG 264
 |||||

QY 277 ATTCTGGGCCAGGACAGACAGGCGCTACTCTGGAGAGGAGTCCCTGCAAGCTGCAGCAG 336
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 DB 265 ATCCGTGCCAAACAGAACAGGAGTACCTCTGGAGAGGAGTCCCTCCCGAGCAGCTGAAACGG 324
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 QY 337 TTCTCTGAGCTGGGAGAGGTGTTTGGACCAACAAGTGCCTCTTTTGGTGAAGGTGACA 396
 |||||
 DB 325 CTCTCTGGAGCTGGGAGAGGCGTCTCTGGGACAGCAAGTGCCTACTTTTGGTGAAGTGA 384
 |||||
 QY 397 CATCATGTGACCTCTTTCAGTGACCATCTACGGTGTGGGCTTGAACCTACTACCCCCAG 456
 |||||
 DB 385 CGCCTCTGGGCTCTACGGGACCTCTTAAAGTGTGAGGCTCTGGACTCTTCTCCCCAG 444
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 QY 457 AACATCACCATGA 469
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 DB 445 AACATCACTATGA 457
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RESULT 13
 BE995172
 LOCUS
 DEFINITION UI-M-CGOp-bil-h-10-0-UI.s1 NIH BMAP Ret4_S2 Mus musculus cDNA clone
 UI-M-CGOp-bil-h-10-0-UI 3', mRNA sequence.
 ACCESSION BE995172
 VERSION BE995172.1 GI:10679153
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 455)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mEST@mail.nih.gov
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
 clones from RESEARCH GENETICS. It should be noted that Bento Soares
 is generating a small number of additional specialized
 non-redundant arrays of BMAP cDNAs whose availability will be
 considered under appropriate and limited collaborative arrangements
 The tissue for this library was contributed by Dr. Xin-Yuan Fu,
 Yale University School of Medicine The following repetitive
 elements were found in this cDNA sequence: 1-31,
 >(CAG)n#Simple repeat
 Seq primer: M13 Forward
 POLYA=No.

FEATURES
 Location/Qualifiers
 1..455
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CGOp-bil-h-10-0-UI"
 /lab_host="DHI08 (Life Technologies)"
 /clone_lib="NIH BMAP Ret4_S2"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH BMAP Ret4_S2 library is a subtracted library,
 ultimately derived from mouse retina tissue libraries at
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue
 for this library was contributed by Dr. Xin-Yuan Fu, Yale

University School of Medicine
TAG SEQ=None found"

ORIGIN	Query Match	41.3%	Score 248.4;	DB 2;	Length 455;
	Best Local Similarity	79.5%;	Pred. No. 5.1e-57;		
	Matches 294;	Conservative 0;	Mismatches 76;	Indels 0;	Gaps 0
Qy	97	GAGTCCACACCCCTGCAGGTCATCCTGGGCTGTGNAATGCAAGAGACAAACAGTACCCGAG	156		
Db	86	GAGTCCACACATCCTGCAGGTCGGTCCTAGGCTGTGAGGTGCATGAAGAACAAGTACCAGC	145		
Qy	157	GGCTACTGGAAGTAGTCGGGTATGATGGGAGGACCACTTGTGAATTCGCGCTTGACACACTG	216		
Db	146	GGCTTCCTGGAGATATGTTATGACGGGCAAGATCACCTGGAAATTCGCCCAAGACACTA	205		
Qy	217	GATTGGAGAGCAGCAGAAACCCAGGGCCTGGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAAG	276		
Db	206	AACTGGAGCGCAGCCGACCCAGGGGCCTGGGCCCAACCAAGGTGGAAATGGGACGAGCACAAG	265		
Qy	277	ATTCGGGCCAGGCAGAACAGAGGCCTTACTCTGGAGAGGGACTGCGCTGCACAGCTGCAGCAG	336		
Db	266	ATCCGTGCCAAACAGAACAGGGACTACTCTGGAGAGGACTGCCCGCAGCAGCTGAAACGG	325		
Qy	337	TTCCTGGAGCTGGGGAGAGGTGTTTTTGGACCAACAAAGTGCCTCTCTTTGGTGAAGGTGACA	396		
Db	326	CTCCTGGAGCTGGGGAGAGGGGTTCTGGGACAGCAAGTGCCTTACTTTGGTGAAGTGAAT	385		
Qy	397	CATCATGTGACCTCTTCAGTCAGTCACCACTCTACGGTCTCGGGCCTTCGAATCTACTTACCCCCAG	456		
Db	386	CGCCACTGGGCTCTACGGGACCTCTCTAAGGTGTAGGCTCTAGGCTCTCTTCTCCCCAG	445		
Qy	457	AACATCACCA	466		
Db	446	AACATCACTA	455		

RESULT 14	CA569584	542 bp	linear	EST 19-NOV-2002
LOCUS	CA569584			
DEFINITION	K0445A07-5N NIA Mouse Mesenchymal Stem Cell cDNA Library (long)			Mus musculus cDNA clone NIA:K0445A07 IMAGE:30063366 5', mRNA sequence.
ACCESSION	CA569584			
VERSION	CA569584.1	GI:25114271		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	1. (bases 1 to 542)			
JOURNAL	Pao,Y., Kargul,G.D., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,			
COMMENT	Umezawa,A. and Ko,M.S.H.			
	Systematic Analyses of NIA Mouse Mesenchymal Stem Cell cDNA Library			
	(Long)			
	Unpublished (2001)			
	Contact: ESIS: K0445A07-3			
	Contact: Dawood B. Dudekula			
	Laboratory of Genetics			
	National Institute on Aging/National Institutes of Health			
	333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA			
	Email: cdna@lgsun.grc.nia.nih.gov			
	Plate: K0445 row: A column: 07			
	Seq primer: M13 Reverse			
	High quality sequence stop: 542			
FEATURES	POLYA=No.			
source	Location/Qualifiers			
	1. 542			
	/organism="Mus musculus"			
	/mol_type="mRNA"			
	/strain="C3H/He"			
	/db_xref="niaEST:K0445A07-5N"			
	/db_xref="taxon:10090"			
	/clone="NIA:K0445A07 IMAGE:30063366"			

FEATURES

RESULT 15
BF883952/c
LOCUS
DEFINITION
ACCESSION
VERSION

BF883952 384 bp mRNA linear EST 17-JAN-2001
PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.
BF883952
BF883952.1 GI:12274078

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/tissue_type="Mesenchymal stem cell"
/cell_line="9-15-C cells"
/lab_host="DH10B"
/clone_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library
(Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Dr. Akihito Umezawa (Keto University School
of Medicine, Japan). Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-GCACGATCTTGATCGGCGGGCGGCCCTTTTCTTTT-3'] from
2.2 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker L1-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA)."

```

ORIGIN

Query Match	40.7%;	Score	244.6;	DB	6;	Length	542;
Best Local Similarity	76.7%;	Pred. No.	6e-56;				
Matches	323;	Conservative	0;	Mismatches	74;	Indels	24;
Gaps	1;						

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[illegible]

FEATURES source

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Best Local Similarity	100.0%;	Pred. No. 5.5e-52;		
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QY	121	CTGGGCTGTGAAATGCAAGAAGACACAGTACCGAGGGCTACTGGAGTAGTCGGGTATGAT	180	
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DB	65	GGCAGGACCACTTGAATTTCTGCCCTGCACACACTGGATTGGAGAGCAGC	16	

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Job time : 1900.7 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-497-957-9_COPY_465_1065

Perfect score: 601
Sequence: 1 CAGATGCTGCTGCAGCTGAG.....GGAAGAGCAGAGATATACGT 601

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	601	100.0	1440	3	US-08-652-265-12
5	601	100.0	1440	3	US-08-834-497A-9
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7	601	100.0	1440	3	US-08-834-497A-11
8	601	100.0	1440	3	US-08-834-497A-12
9	601	100.0	1440	3	US-09-503-444A-9
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44	232	38.6	517	3	US-09-503-444A-20
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ALIGNMENTS

RESULT 1
US-08-652-265-9
; Sequence 9, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; NAME/KEY: allele
; LOCATION: replace (408, "c")

OTHER INFORMATION: /phenotype= "normal or wild-type"
OTHER INFORMATION: (unaffected)
FEATURE: /label= 24d2
NAME/KEY: allele
LOCATION: replace (414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type"
OTHER INFORMATION: (unaffected)
FEATURE: /label= 24d7
NAME/KEY: allele
LOCATION: replace (1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type"
OTHER INFORMATION: (unaffected)
FEATURE: /label= 24d1
US-08-652-265-9

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175; Mismatches 0; Indels 0; Gaps 0;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 TACCTGGAGAGGACTGCGCTGCACAGCTGCAGAGTTCCTGGAGCTGGGGAGAGGTGT 360
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DB 1065 T 1065

RESULT 2
US-08-652-265-10
Sequence 10, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.

APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
NAME/KEY: allele
LOCATION: replace (1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
US-08-652-265-10

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175; Mismatches 0; Indels 0; Gaps 0;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 465 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCTCATCTGTGAC 524
QY 61 TTCTGGACTATTATGAAATACAAACACAGAGAGTCCACACCCCTGCAGGTATC 120
DB 525 TTCTGGACTATTATGAAATACAAACACAGAGAGTCCACACCCCTGCAGGTATC 584
QY 121 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
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RESULT 3

US-08-652-265-11
; Sequence 11, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gairke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele

; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d2
US-08-652-265-11
Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 465 CAGATGTGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTGTGAC 524
QY 61 TTCTGACACTATTATGAAATCACAACACAGCAAGAGTCCCAACCCCTGCAAGTCAATC 120
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QY 301 TACCTGGAGAGGGAGTGCCTCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGT 360
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US-08-652-265-12
; Sequence 12, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gairke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

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; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
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; FEATURE:
; NAME/KEY: allele
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; OTHER INFORMATION: /label= 24d1
; US-08-652-265-12

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 481 GATAAGCAGCCAAATGGATGCCAAGAGTTCCAAACCTAAAGAGTATTGCCCAATGGGGAT 540
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RESULT 5
US-08-834-497A-9
; Sequence 9, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Teuchihasi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
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Db 1065 T 1065

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US-08-834-497A-12
; Sequence 12, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: CDNA
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; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d2
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d1
; US-08-834-497A-12

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2,8e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGCTGAGTGTGAGTCTGAAAGGTGGATCACAATGTTCACTGTGAC 60
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Db 585 CTGGGCTGTGAAATGCAAGACAGTACCGAGGCTACTTGGAAAGTACGGGTATGAT 644
QY 181 GGGCAGGACCACTTGAATTTGCCCTTGACACACTGGATTGGAGAGCAGACAGCCAGG 240
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QY 361 TTGACCAACAAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGACC 420
Db 825 TTGACCAACAAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGACC 884
QY 421 ACTCTACGGTGTGGGCTTGAACCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 480
Db 885 ACTCTACGGTGTGGGCTTGAACCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 944
QY 481 GATAAGCAGCAATGATGCAAGGATTCGAACCTAAAGACGATATGCCCAATGGGAT 540
Db 945 GATAAGCAGCAATGATGCAAGGATTCGAACCTAAAGACGATATGCCCAATGGGAT 1004
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Db 1005 GGGACCTACACGGGCTGGATAACCTTGGCTGTACCCCTCGGGAAGACAGATATACG 1064
QY 601 T 601
Db 1065 T 1065

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US-09-503-444A-9
; Sequence 9, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.

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; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Teuchiashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "c")
; OTHER INFORMATION: /phenotype= "normal or wild-type"
; OTHER INFORMATION: (unaffected)
; OTHER INFORMATION: /label= 24d2
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(414, "a")
; OTHER INFORMATION: /phenotype= "normal or wild-type"
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; FEATURE:
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; LOCATION: replace(1066, "g")
; OTHER INFORMATION: /phenotype= "normal or wild-type"
; OTHER INFORMATION: (unaffected)
; OTHER INFORMATION: /label= 24d1
;
; US-09-503-444A-9

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Query Match 100.0%; Score 601; DB 3; Length 1440;
 Best Local Similarity 100.0%; Pred. No. 2.8e-175;

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Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||
QY 465 CAGATGTGGCTGCAGCTCAGTCTGAAAGGGTGGGATCAATGTTCACTGTTGAC 524
Db |||||
QY 61 TTCTGGACTATTATGGAAGTCAACACACAGCAGGAGTCCACACCTCGCAGGTCATC 120
Db |||||
QY 525 TTCTGGACTATTATGGAAGTCAACACACAGCAGGAGTCCACACCTCGCAGGTCATC 584
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QY 645 GGGCAGGACCACTTTGAAATTCGCCCTGACACATCTGGATTGGAGAGCAGAGAACCCAGG 704
Db |||||
QY 241 GCCTGGCCCAACAGCTGGAGTGGGAAAGGACACAGATTTCGGGCCAGGACAGAGGGCC 300
Db |||||
QY 705 GCCTGGCCCAACAGCTGGAGTGGGAAAGGACACAGATTTCGGGCCAGGACAGAGGGCC 764
Db |||||
QY 301 TACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGT 360
Db |||||
QY 765 TACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGT 824
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QY 361 TTGGACCAACAGTGCCTCTTTGGTGAAGTGACACATCATGTGACCTTTCAGTGACC 420
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QY 825 TTGGACCAACAGTGCCTCTTTGGTGAAGTGACACATCATGTGACCTTTCAGTGACC 884
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QY 421 ACTCTACCGTGTCCGGCCCTTGAACCTACTACCCCAAGACATCACCATTGAAGTGGCTGAAG 480
Db |||||
QY 885 ACTCTACCGTGTCCGGCCCTTGAACCTACTACCCCAAGACATCACCATTGAAGTGGCTGAAG 944
Db |||||
QY 481 GATAAGCAGCAATGGATGCCAAGAGTTCGAACCTTGAAGAGCTATTGCCCAATGGGAT 540
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QY 601 T 601
Db 1065 T 1065

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RESULT 10
US-09-503-444A-10
; Sequence 10, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Teuchiashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION:
; OTHER INFORMATION: /label= 24d1
;
US-09-503-444A-10

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175; Mismatches 0; Indels 0; Gaps 0;
Matches 601; Conservative 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
QY 61 TTCTGCACTATTATGGAATAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC 120
DB 525 TTCTGCACTATTATGGAATAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCAGGGGTCTCTGGAAGTACCGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGCAACAGTACCAGGGGTCTCTGGAAGTACCGGTATGAT 644
QY 181 GGCAGGACACACCTTCAATTTCTCCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 240
DB 645 GGCAGGACACCTTCAATTTCTCCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 704
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTGGGCCAGGCAAGAGCCAGG 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTGGGCCAGGCAAGAGCCAGG 764
QY 301 TACCTGGAGAGGAGTGCCTCTGCACAGCTGCACAGTTCGTGGAGCTGGGGAGGTGT 360
DB 765 TACCTGGAGAGGAGTGCCTCTGCACAGCTGCACAGTTCGTGGAGCTGGGGAGGTGT 824
QY 361 TTGGACCAACAAGTGCCTCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420
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QY 421 ACTCTACGGTGTGGGGCTTTGAACTACTACCCCAAGAACATCACACCAATGAAGTGGCTGAAG 480
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QY 481 GATAAGCAGCCCAATGGATGCAAGAGGATTCGAACCTTAAAGACCTATTGGCCCAATGGGGAT 540
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DB 1005 GGGACCTACAGGGCTGGGATACCTTTGGGTGTACCCCTGGGGAAGAGCAGAGATATACG 1064
QY 601 T 601
DB 1065 T 1065

RESULT 11
US-09-503-444A-11
; Sequence 11, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
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; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
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; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d2
; US-09-503-444A-11

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGATCACAATGTTCACTGTTGAC 60
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QY 61 TTCTGGACTATTATGAAATCACAACACAGCAAGAGGATCCACACCCCTGCAGGTCAATC 120
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QY 181 GGGCAGGACCACTTGAATTTGCTGCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
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DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGAACAGGGCC 764
QY 301 TACCTGGAGAGGACTGCTGCTGCAAGCTGAGAGTGGTGGAGCTGGGGAGAGGTGTT 360
DB 765 TACCTGGAGAGGACTGCTGCTGCAAGCTGAGAGTGGTGGAGCTGGGGAGAGGTGTT 824
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DB 945 GATAGCAGCAATGATGCCAAGAGTTCGAACCTTAAGAGCTATTGCCCAATGGGAT 1004
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DB 1065 T 1065

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RESULT 12

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US-09-503-444A-12
; Sequence 12, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas

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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
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; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d2
; FEATURE:
; NAME/KEY: allele
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; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d1
; US-09-503-444A-12

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Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGATCACAATGTTCACTGTTGAC 524
QY 61 TTCTGGACTATTATGAAATCACAACACAGCAAGAGGATCCACACCCCTGCAGGTCAATC 120
DB 525 TTCTGGACTATTATGAAATCACAACACAGCAAGAGGATCCACACCCCTGCAGGTCAATC 584
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QY 181 GGGCAGGACCACTTGAATTTGCTGCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
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Qy	481	GATAAGCAGCCAAATGGATGCCAAGGAGTTCGAACCTAAAGACGCTATTGCCCAATGGGGAT		540
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Qy	541	GGGACCTACAGGGCTGGATAAACCCTTGGCTGTACCCCTCTGGGGAAGACAGAGATATACG		600
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; Sequence 1, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277,457
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; - OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-277-457-1

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QY	301	TACCTGGAGGGG	ACTGCCCTGGCAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGTT	360	
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QY	421	ACTCTACGGT	TCGGGGCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAG	480	
Db	664	ACTCTACGGT	TCGGGGCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAG	723	
QY	481	GATAAGCAGCCA	TAATGGATGTCAGAGGTTTCGAACCTTAAGACGTATTTCGCCAATGGGGAT	540	
Db	724	GATAAGCAGCCA	TAATGGATGTCAGAGGTTTCGAACCTTAAGACGTATTTCGCCAATGGGGAT	783	
QY	541	GGGACCTACC	AGGGCTGGATAA	CTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG	600
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; Patent No. 6509442					
; GENERAL INFORMATION:					
; APPLICANT: Rothenberg, Barry E.					
; APPLICANT: Sawada-Hirai, Ritsuko					
; APPLICANT: Barton, James C.					
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS					
; FILE REFERENCE: 24065-004 DIV					
; CURRENT APPLICATION NUMBER: US/09/679,729					
; CURRENT FILING DATE: 2000-10-04					
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; PRIOR FILING DATE: 1999-03-26					
; NUMBER OF SEQ ID NOS: 30					
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; SEQ ID NO 1					
; LENGTH: 2506					
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; ORGANISM: Homo Sapiens					
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US-09-679-729-1					

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; Sequence 1180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1180
; LENGTH: 2717
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1180
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Query Match 100.0%; Score 601; DB 4; Length 2717;
Best Local Similarity 100.0%; Pred. No. 4e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      121 CTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT 180
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Qy      301 TACCTGGAGAGGACTGCCCTCGACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 360
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Db      885 ACTCTACGGTGTGGGCCCTTGAACCTACTACTACCCCCCAGAACATCACCATTGAAGTGGCTGAAG 944
Qy      481 GATAAGCAGCCAATGATGCCAAGGAGTTGGAACCTTAAAGACGTATTGCCCCAATGGGGAT 540
Db      945 GATAAGCAGCCAATGATGCCAAGGAGTTGGAACCTTAAAGACGTATTGCCCCAATGGGGAT 1004
Qy      541 GGGACCTACACGGCTGGGATAACCTTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600
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Qy      601 T 601
Db      1065 T 1065
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Job time : 96.9625 secs

GenCore version 5.1.6
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Scoring table: IDENTITY NUC

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Searched: 6067389 seqs, 3125258755 residues

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Maximum Match 100%

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3	601	100.0	1440	15	US-10-138-888-11
4	601	100.0	1440	15	US-10-138-888-12
5	601	100.0	1440	15	US-10-138-888-77
6	601	100.0	2506	10	US-09-981-606-1
7	601	100.0	2739	21	US-10-956-250-1

Sequence 271, Ap	2285	21	US-10-741-600-271
Sequence 269, Ap	2426	21	US-10-741-600-269
Sequence 265, Ap	2716	21	US-10-741-600-265
Sequence 267, Ap	2674	21	US-10-741-600-267
Sequence 264, Ap	2231	21	US-10-741-600-264
Sequence 268, Ap	2189	21	US-10-741-600-268
Sequence 23829, A	282	16	US-10-029-386-23829
Sequence 10129, A	500	16	US-10-029-386-10129
Sequence 3112, Ap	5749	9	US-09-764-877-3112
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Sequence 25, Appl	5982	13	US-10-016-634A-25
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GENERAL INFORMA	10825	15	US-10-138-888-3
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Sequence 27, Appl	12146	10	US-09-981-606-27
Sequence 1, Appl	235033	15	US-10-301-844-1
Sequence 2, Appl	237326	15	US-10-301-844-2
Sequence 17631, A	21608	21	US-10-741-600-17631
Sequence 105, Ap	596	17	US-10-158-057-105
Sequence 20, Appl	517	15	US-10-138-888-20
Sequence 21, Appl	517	15	US-10-138-888-21
Sequence 266, Ap	2009	21	US-10-741-600-266
Sequence 261, Ap	2440	21	US-10-741-600-261
Sequence 263, Ap	1955	21	US-10-741-600-263
Sequence 7420, Ap	201	21	US-10-741-600-7420
Sequence 7429, Ap	201	21	US-10-741-600-7429
Sequence 7440, Ap	201	21	US-10-741-600-7440
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Sequence 7442, Ap	201	21	US-10-741-600-7442
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Sequence 7503, Ap	201	21	US-10-741-600-7503

ALIGNMENTS

RESULT 1

US-10-138-888-9
; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/138,888
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
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; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; (HH)"
; /label= 24d1
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10

Query Match 100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1065 T 1065
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; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
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; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian M. Poissant
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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; /label= 24d2
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US-10-138-888-11

Query Match 100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1065 T 1065
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; Sequence 12, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
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APPLICANT: Thomas, Winston J.
           Drayna, Dennis T.
           Feder, John N.
           Gnirke, Andreas
           Ruddy, David
           Teuchihaashi, Zenta
           Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
```

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
```

```
;
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; (HH)"
; /label= 24d2
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; (HH)"
; /label= 24dl
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-138-888-12
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Query Match 100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
Db 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
Qy 61 TTCTGGACTATTATGGAATAATCAAAACACAGCAAGAGTCCACACCCCTGCAGGTGATC 120
Db 525 TTCTGGACTATTATGGAATAATCAAAACACAGCAAGAGTCCACACCCCTGCAGGTGATC 584
Qy 121 CTGGGCTGTGAAATCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT 180
Db 585 CTGGGCTGTGAAATCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT 644
Qy 181 GGGCAGGACCACTTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 240
Db 645 GGGCAGGACCACTTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 704
Qy 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGAGCAACAGGGCC 300
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGAGCAACAGGGCC 764
Qy 301 TACTTGGAGAGGACTGCCCTTGCACAGCTGCAGAGTTCCTGGAGTGGGGAGAGGTGTT 360
Db 765 TACTTGGAGAGGACTGCCCTTGCACAGCTGCAGAGTTCCTGGAGTGGGGAGAGGTGTT 824
Qy 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGCACATCATGTGACCTCTTCAGTGACC 420
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGCACATCATGTGACCTCTTCAGTGACC 884
Qy 421 ACTTACCGTGTGGGCCCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 480
Db 885 ACTTACCGTGTGGGCCCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 944
Qy 481 GATAAGCAGCAATGATGCCAAGAGTTTGGAACTTAAAGAGCTATTGCCCAATGGGGAT 540
Db 945 GATAAGCAGCAATGATGCCAAGAGTTTGGAACTTAAAGAGCTATTGCCCAATGGGGAT 1004
Qy 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600
Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064
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QY 601 T 601
 Db 1065 T 1065

RESULT 5
 US-10-138-888-77
 ; Sequence 77, Application US/10138888
 ; Publication No. US20030148972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Winston J.
 ; Drayna, Dennis T.
 ; Feder, John N.
 ; Gnirke, Andreas
 ; Ruddy, David
 ; Tsuchihashi, Zenta
 ; Wolff, Roger K.
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/138,888
 ; FILING DATE: 02-May-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,497
 ; FILING DATE: 04-APR-1997
 ; APPLICATION NUMBER: US 08/652,265
 ; FILING DATE: 23-MAY-1996
 ; APPLICATION NUMBER: US 08/632,673
 ; FILING DATE: 16-APR-1996
 ; APPLICATION NUMBER: US 08/630,912
 ; FILING DATE: 04-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brian M. Poissant
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 8907-095-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; INFORMATION FOR SEQ ID NO: 77:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1440 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 222..1268
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: replace(414, "c").
 ; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis (HH)"
 ; /label= 24d7
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
 US-10-138-888-77

Query Match 100.0%; Score 601; DB 15; Length 1440;
 Best Local Similarity 100.0%; Pred. No. 5.8e-184;
 Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
 |||||
 Db 465 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
 |||||

QY 61 TTCTGGACTATTATGGAAATCAACAACAGCAAGAGAGTCCACACCCCTGCAGGTATC 120
 |||||
 Db 525 TTCTGGACTATTATGGAAATCAACAACAGCAAGAGAGTCCACACCCCTGCAGGTATC 584
 |||||

QY 121 CTGGGCTGTGAAATGCAAGAGACAACAGTACCGAGGGCTACTTGGAGTACGGGTATGAT 180
 |||||
 Db 585 CTGGGCTGTGAAATGCAAGAGACAACAGTACCGAGGGCTACTTGGAGTACGGGTATGAT 644
 |||||

QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG 240
 |||||
 Db 645 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG 704
 |||||

QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 300
 |||||
 Db 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 764
 |||||

QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTCGTGGAGCTGGGGAGAGGTGT 360
 |||||
 Db 765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTCGTGGAGCTGGGGAGAGGTGT 824
 |||||

QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGCAC 420
 |||||
 Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGCAC 884
 |||||

QY 421 ACTTACGGTGTGGGCCCTTGAACACTACTACCCCAAGAACATCAACCATGAAGTGGCTGAAG 480
 |||||
 Db 885 ACTTACGGTGTGGGCCCTTGAACACTACTACCCCAAGAACATCAACCATGAAGTGGCTGAAG 944
 |||||

QY 481 GATAAGCAGCAATGATGCCAAGAGTTCGAACCTTAAAGACCTATTGCCCAATGGGGAT 540
 |||||
 Db 945 GATAAGCAGCAATGATGCCAAGAGTTCGAACCTTAAAGACCTATTGCCCAATGGGGAT 1004
 |||||

QY 541 GGGACCTACAGGGCTGGATAACCTTTGGTGTACCCCTGGGGAAGAGCAGATATACG 600
 |||||
 Db 1005 GGGACCTACAGGGCTGGATAACCTTTGGTGTACCCCTGGGGAAGAGCAGATATACG 1064
 |||||

QY 601 T 601
 Db 1065 T 1065

RESULT 6
 US-09-981-606-1
 ; Sequence 1, Application US/09981606
 ; Publication No. US20030129595A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothenberg et al.
 ; TITLE OF INVENTION: Mutations associated with iron disorders
 ; FILE REFERENCE: 24065-004CON
 ; CURRENT APPLICATION NUMBER: US/09/981,606
 ; CURRENT FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: 09/277,457
 ; PRIOR FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2506
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-981-606-1

Query Match 100.0%; Score 601; DB 10; Length 2506;
 Best Local Similarity 100.0%; Pred. No. 7.1e-184;
 Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
 |||||

Db 244 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGARAAGGGTGGATCATCATGTTCACTGTTGAC 303
QY 61 TTCTGGACTATTATGAAATATCAACCAACAGAGAGTCCACACACCTTCAGGTGATC 120
Db 304 TTCTGGACTATTATGAAATATCAACCAACAGAGAGTCCACACACCTTCAGGTGATC 363
QY 121 CTGGCTGTGAATGCAAGACACACAGTACCGAGGGCTACTGAGTACGGGTATGAT 180
Db 364 CTGGCTGTGAATGCAAGACACACAGTACCGAGGGCTACTGAGTACGGGTATGAT 423
QY 181 GGGCAGGACACCTGTAATTTCTGCTGACACACTGGATTGGAGAGCAGACAGAACCCAGG 240
Db 424 GGGCAGGACACCTGTAATTTCTGCTGACACACTGGATTGGAGAGCAGACAGAACCCAGG 483
QY 241 GCTGGCCCAACCAAGCTGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGAACCCAGG 300
Db 484 GCTGGCCCAACCAAGCTGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGAACCCAGG 543
QY 301 TACCTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGT 360
Db 544 TACCTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGT 603
QY 361 TTGGACCAACAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 604 TTGGACCAACAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 563
QY 421 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 480
Db 664 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 723
QY 481 GATAAGCAGCAATGATGCCAGGAGTTCGAACTTAAAGAGTATTCGCCCAATGGGGAT 540
Db 724 GATAAGCAGCAATGATGCCAGGAGTTCGAACTTAAAGAGTATTCGCCCAATGGGGAT 783
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGAGATATAG 600
Db 784 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGAGATATAG 843
QY 601 T 601
Db 844 T 844

RESULT 7
US-10-956-250-1
; Sequence 1, Application US/10956250
; Publication No. US20050090430A1
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; Schatzman, Randall C.
; Tsuchihashi, Zenta
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
; ISEASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/956,250
; FILING DATE: 01-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,559

; FILING DATE: 27-Aug-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/866,211
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0062-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2739 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-10-956-250-1
; Query Match 100.0%; Score 601; DB 21; Length 2739;
; Best Local Similarity 100.0%; Pred. No. 7.3e-184;
; Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
Db 477 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 536
QY 61 TTCTGGACTATTATGAAATATCAACCAACAGCAGAGGAGTCCACACCTTCAGGTGATC 120
Db 537 TTCTGGACTATTATGAAATATCAACCAACAGCAGAGGAGTCCACACCTTCAGGTGATC 596
QY 121 CTGGCTGTGAAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
Db 597 CTGGCTGTGAAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 656
QY 181 GGGCAGGACCAACCTTTGAAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 240
Db 657 GGGCAGGACCAACCTTTGAAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 716
QY 241 GCTGGCCCAACCAAGCTGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGAACCCAGG 300
Db 717 GCTGGCCCAACCAAGCTGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGAACCCAGG 776
QY 301 TACCTGGAGAGGAGTGCCTGCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGT 360
Db 777 TACCTGGAGAGGAGTGCCTGCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGT 836
QY 361 TTGGACCAACAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 837 TTGGACCAACAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 896
QY 421 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 480
Db 897 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 956
QY 481 GATAAGCAGCAATGATGCCAGGAGTTCGAAACCTTAAAGAGTATTCGCCCAATGGGGAT 540
Db 957 GATAAGCAGCAATGATGCCAGGAGTTCGAAACCTTAAAGAGTATTCGCCCAATGGGGAT 1016
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGAGATATAG 600
Db 1017 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGAGATATAG 1076
QY 601 T 601
Db 1077 T 1077

RESIST. 8

US-10-741-600-271
; Sequence 271, Application US/10741600
; Publication No. US20050026169A1

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

RESIST 9

US-10-741-600-269
; Sequence 269, Application US/10741600
; Publication No. US20050026169A1

```

; APPLICANT: CARGILL, Michele et al.
;
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;
; FILE REFERENCE: CL001499

```

RECIT 10

US-10-741-600-265
; Sequence 265, Application US/10741600
; Publication No. US20050026169A1

GENERAL INFORMATION: APPLICANT, CARROLL MICHAEL

APPLICANT: CARGILL, MICHELE et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-265

Query Match      99.7%; Score 599; DB 21; Length 2716;
Best Local Similarity 99.2%; Pred. No. 3.2e-183;
Matches 596; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGTGTGAGAGGCTGGGATCAGATCTGAAAGGGTGGGATCAGATCTTCACTTTGAC 60
DB 465 CAGATGTGGCTGCAGTGTGAGAGGCTGGGATCAGATCTGAAAGGGTGGGATCAGATCTTCACTTTGAC 524

QY 61 TTCTGGACTATTATGGAATAATCAACAACAGCAAGAGGAGTCCACACCTCGCAGGTTCATC 120
DB 525 TTCTGGACTATTATGGAATAATCAACAACAGCAAGAGGAGTCCACACCTCGCAGGTTCATC 584

QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 644

QY 181 GGGCAGGACCACTTGAATTTGCGCTTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTGCGCTTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 704

QY 241 GCCTGCCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGCAAGGGCC 300
DB 705 GCCTGCCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGCAAGGGCC 764

QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGCTGGGGAGAGGTGT 360
DB 765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGCTGGGGAGAGGTGT 824

QY 361 TTGGACCAACAAGTGCCTCTTGGTGAAGGTGACACATCATCTTCAGTGACC 420
DB 825 TTGGACCAACAAGTGCCTCTTGGTGAAGGTGACACATCATCTTCAGTGACC 480

QY 421 ACTCTACGGTGTGGGGCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 480
DB 885 ACTCTACGGTGTGGGGCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 944

QY 481 GATAAGCAGCCAATGGATGCCAAGAGTTGCAACCTTAAAGACGTATTGCCCAATGGGGAT 540
DB 945 GATAAGCAGCCAATGGATGCCAAGAGTTGCAACCTTAAAGACGTATTGCCCAATGGGGAT 1004

QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 600
DB 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATAYG 1064

QY 601 T 601
DB 1065 T 1065
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RESULT 11
US-10-741-600-267
; Sequence 267, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 2674
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-267

Query Match      84.0%; Score 505; DB 21; Length 2674;
Best Local Similarity 92.2%; Pred. No. 9.8e-153;
Matches 554; Conservative 5; Mismatches 0; Indels 42; Gaps 1;

QY 1 CAGATGTGGCTGCAGTGTGAGAGGCTGGGATCAGATCTTCACTTTGAC 60
DB 465 CAGATGTGGCTGCAGTGTGAGAGGCTGGGATCAGATCTTCACTTTGAC 524

QY 61 TTCTGGACTATTATGGAATAATCAACAACAGCAAGAGGAGTCCACACCTCGCAGGTTCATC 120
DB 525 TTCTGGACTATTATGGAATAATCAACAACAGCAAGAGGAGTCCACACCTCGCAGGTTCATC 584

QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 644

QY 181 GGGCAGGACCACTTGAATTTGCGCTTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTGCGCTTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 704

QY 241 GCCTGCCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGCAAGGGCC 300
DB 705 GCCTGCCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGCAAGGGCC 764

QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGCTGGGGAGAGGTGT 360
DB 765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGCTGGGGAGAGGTGT 824

QY 361 TTGGACCAACAAGTGCCTCTTGGTGAAGGTGACACATCATCTTCAGTGACC 420
DB 825 TTGGACCAACAAGTGCCTCTTGGTGAAGGTGACACATCATCTTCAGTGACC 480

QY 421 ACTCTACGGTGTGGGGCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 480
DB 843 ACTCTACGGTGTGGGGCTTGAATCTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 902

QY 481 GATAAGCAGCCAATGGATGCCAAGAGTTGCAACCTTAAAGACGTATTGCCCAATGGGGAT 540
DB 903 GATAAGCAGCCAATGGATGCCAAGAGTTGCAACCTTAAAGACGTATTGCCCAATGGGGAT 962

QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 600
DB 963 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATAYG 1022

QY 601 T 601
DB 1023 T 1023
```

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RESULT 12
US-10-741-600-264
; Sequence 264, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 2231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-264

Query Match      83.7%; Score 502.8; DB 21; Length 2231;
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QY 277 ATTGGGGCAGCAGACAGGGCCCTACCTGGAGGGAGTGCCTGCGACAGCTGCAGCAG 336
|||
Db 181 ATTGGGGCAGCAGACAGGGCCCTACCTGGAGGGAGTGCCTGCGACAGCTGCAGCAG 240
|||
QY 337 TTGCTGGAGCTGGGAGAGGTGTTTTGGACCAACAAG 373
|||
Db 241 TTGCTGGAGCTGGGAGAGGTGTTTTGGACCAACAAG 277
|||

RESULT 15

US-10-029-386-10129
; Sequence 10129, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10129
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: NT HIT: U91328.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q30201, EVALUE 1.00e-52
; OTHER INFORMATION: EST_HUMAN HIT: BG747345.1, EVALUE 0.00e+00
US-10-029-386-10129

Query Match 46.1%; Score 277; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.6e-79;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 GAGTCCACACCCCTGCAGGTCACTCTGGGCTGTGAAATGCAAGAGACACAGTACCGAG 156
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Db 106 GAGTCCACACCCCTGCAGGTCACTCTGGGCTGTGAAATGCAAGAGACACAGTACCGAG 165
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Db 226 GATTGGAGAGCAGCAGAACCCAGGGGCTGGCCCCACCAAGCTGGAGTGGGAAAGGCACAAG 285
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QY 277 ATTGGGGCAGCAGACAGGGCCCTACCTGGAGAGGAGTGCCTGCGACAGCTGCAGCAG 336
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QY 337 TTGCTGGAGCTGGGAGAGGTGTTTTGGACCAACAAG 373
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Db 346 TTGCTGGAGCTGGGAGAGGTGTTTTGGACCAACAAG 382
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Search completed: June 23, 2005, 06:38:40
Job time : 349.016 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:24:18 ; Search time 21352.4 Seconds
(without alignments)
11346.531 Million cell updates/sec

Title: US-09-497-957-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 TCTAAGGTTGAGATAAAATT.....GCTAATTGGAAGGCTGAGGC 5000

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5000	100.0	10825	6	AR117789 Sequence
2	5000	100.0	10825	6	AR117790 Sequence
3	5000	100.0	10825	6	AR149459 Sequence
4	5000	100.0	10825	6	AR149460 Sequence
5	5000	100.0	246240	6	AR036572 Sequence
6	5000	100.0	246240	6	AR036573 Sequence
7	5000	100.0	246240	6	AR036574 Sequence
8	4998.4	100.0	10825	6	AR117791 Sequence
9	4998.4	100.0	10825	6	AR117792 Sequence
10	4998.4	100.0	10825	6	AR149461 Sequence
11	4998.4	100.0	10825	6	AR149462 Sequence
12	4988	99.8	235033	6	BD084121 Polymorph
13	4988	99.8	246282	9	HS091328 Human hered
14	4958.8	99.2	237326	6	BD084122 Polymorph
15	4957.2	99.1	12146	6	AR199263 Sequence
16	4957.2	99.1	12146	6	AR275782 Sequence
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18	4888.8	97.8	11214	9	AF447807 Pan trogl
19	4858.2	97.2	193752	2	AL359892 Homo sapi

20	4607.8	92.2	5982	6	AX701831 Sequence
21	2556.4	51.1	8622	6	AX347044 Sequence
22	2248.8	45.0	8622	6	AX347045 Sequence
23	1071.8	21.4	1865	9	AK123489 Homo sapi
24	832.2	16.6	874	9	Y09800 H.sapiens H
25	740.2	14.8	3334	4	AF301591 Ceratophe
26	657	13.1	761	9	Y09801 H.sapiens H
27	562.2	11.2	4349	4	AF301592 Dicerob b
28	360	7.2	3043	9	AF204869 Homo sapi
29	337.4	6.7	129225	9	AC026765 Homo sapi
30	332.6	6.7	177273	9	AC074194 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AR117789 10825 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6140305.
ACCESSION AR117789
VERSION AR117789.1 GI:14098695
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z., and Wolff,R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 1 31-OCT-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Parent
clms to polypeptide:

Query Match	100.0%;	Score	5000;	DB	6;	Length	10825;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	5000;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATATAATTTA	60				
Qy	61	AATATCTAAAGTTTCAGATCAGAACATTGCGAGCTACTTTTCCCAATCAACACCCCT	120				
Db	61	AATATCTAAAGTTTCAGATCAGAACATTGCGAGCTACTTTTCCCAATCAACACCCCT	120				
Qy	121	TCAGATTAAACCAAGGGGACACTGGATCAGTGTGTTTTCACAGCAGGTACCTT	180				
Db	121	TCAGATTAAACCAAGGGGACACTGGATCAGTGTGTTTTCACAGCAGGTACCTT	180				
Qy	181	CTGCTGTAGGAGAGAGAGAACTAAAGTCTTGAAGACCTGTGCTTTTCCACGAGAGTT	240				
Db	181	CTGCTGTAGGAGAGAGAGAACTAAAGTCTTGAAGACCTGTGCTTTTCCACGAGAGTT	240				
Qy	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTTGGAGCCATCCCCG	300				

Db 241 TTAGTGGGCACTCTCGAGCTAGCAATAGCTGTAGGGTGAATCTCTGGAGCCATCCCG 300
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Db 361 ATGGGCGCGGAGCCAGGCGCGGCTCTCTCTCTGATGCTTTTGCAGACCGCGTCTG 420
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Db 4981 GCTAATTTGGAAGGCTGAGGC 5000

RESULT 2
AR117790
LOCUS AR117790 10825 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6140305.
ACCESSION AR117790
VERSION AR117790.1 GI:14098696
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 3 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..10825
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 5000; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 4201 TGGTTGCAAGTTAAACAGGCTGGGATTTTTCAGAGTCCCAACACCTGCAAGTCACTCTG 4260
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DB 4261 GGCTGTGAATGCAAGAGAACACAGTACCCAGGCTACTGGAAGTACGGGTATGATGG 4320
QY 4321 CAGGACCACTTTGAATTTCTGCCCTGACACACTGGAATTTGAGAGCAGCAGAAACCCAGGGCC 4380
DB 4321 CAGGACCACTTTGAATTTCTGCCCTGACACACTGGAATTTGAGAGCAGCAGAAACCCAGGGCC 4380
QY 4381 TGGCCCAACAGCTGGAGTGGGAAAGGCAAGATTTGGGGCAGGCAAGACAGGSCCTAC 4440
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DB 4441 CTGGAGGGGACTGCCCTGACAGCTGAGCAGTGTCTGAGCTGGGAGGCTGTTTGG 4500
QY 4501 GACCAACAGGATATGTTGGAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
DB 4501 GACCAACAGGATATGTTGGAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
QY 4561 AGGTTGACAGGCAAGGAAATCCCTGGTGGAGTTTTCAGAGGTTGAGGCTGTGTGCTC 4620
DB 4561 AGGTTGACAGGCAAGGAAATCCCTGGTGGAGTTTTCAGAGGTTGAGGCTGTGTGCTC 4620
QY 4621 TCCAAATTTCTGGAAGGAGCTTTCTCAATCTAGAGTCTACCTTATAATTTGAGATGTA 4680
DB 4621 TCCAAATTTCTGGAAGGAGCTTTCTCAATCTAGAGTCTACCTTATAATTTGAGATGTA 4680
QY 4681 TGAGACAGCCACAGTCAATGGGTTTAAATTTCTTCTCCATGCAATATCGCTCAAAAGGAA 4740

1441	Db	 TGTAGCACAGTGTGTTCTGTGGGTACACGCGCGCTCAGCAGCACATTTTGAGTTTGGTA	1500
1501	Qy	 CTACGTGTATCCACATTTTACACATGACAAGAATGAGCGCATGGCAGCGCTGTTCTCTGG	1560
1501	Db	 CTACGTGTATCCACATTTTACACATGACAAGAATGAGCGCATGGCAGCGCTGTTCTCTGG	1560
1561	Qy	 CAAAATTTATTTCAATGGTACACTGGGCTTTTGGTGGCAGAGTCTCATGTCTCCACTTCATAGC	1620
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1981	Qy	 TTGGATTTAAAAAGCGGTTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGGG	2040
1981	Db	 TTGGATTTAAAAAGCGGTTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGGG	2040
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2101	Db	 CCTCCCTACTCACTAGTGTCTAGGAGCACTCCCCAGTCTTTGACAACCAAAAATGTCTCT	2160
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2221	Qy	 AATAAACAAGTAGTGTGGGAGTAGAGGCCAAGAGTAGTAAATGGGCTCAGAGAGGA	2280
2221	Db	 AATAAACAAGTAGTGTGGGAGTAGAGGCCAAGAGTAGTAAATGGGCTCAGAGAGGA	2280
2281	Qy	 GCCACAAAAGGTTGTGACGGGCCCTGTAGGCTGTGCTGTGAATTTAGCCCAAGAGTA	2340
2281	Db	 GCCACAAAAGGTTGTGACGGGCCCTGTAGGCTGTGCTGTGAATTTAGCCCAAGAGTA	2340
2341	Qy	 ACAGTGATCTGTCA CAGGCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAA	2400
2341	Db	 ACAGTGATCTGTCA CAGGCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAA	2400
2401	Qy	 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAGCTGTGTACACAGTCCAGGCAAG	2460
2401	Db	 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAGCTGTGTGTACACAGTCCAGGCAAG	2460
2461	Qy	 AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAAAGGGAGTCACAAAACATTGTCTCTGAA	2520
2461	Db	 AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAAAGGGAGTCACAAAACATTGTCTCTGAA	2520
2521	Qy	 TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTGTGTGAGAGAAAGAGAAATTTGG	2580

Db	2521	TATATTCTGAAGGAAGTTGCTGAAGGATTCATATGTTGTGTGAGAGAAGAGAATAATGG	2581
Qy	2581	CTGGGTGTAGTAGCTCATGCGCAAGAGAGAGCGCCAAAGGAGAGCAGATTCCCTGAGCTCAGGA	2640
Db	2581	CTGGGTGTAGTAGCTCATGCGCAAGAGAGAGCGCCAAAGGAGAGCAGATTCCCTGAGCTCAGGA	2640
Qy	2641	GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA	2700
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Qy	2701	GCTGGGTGTGGTGGCATGCACTGTGTATCTAGTACTCGGGAGGCTGAGGTGAGGGTA	2760
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Db	2821	CTAGGTGACAGACAGCAAGACCCCTGTCTCCCTGAGCCCCCTGAAAAGAGAGATTAAAGT	2880
Qy	2881	TGACTTTGTTCTTTATTTTAAATTTATTTGAGCTGTAGCAGTGGGGTAAATGGCAATGCCAT	2940
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Qy	2941	TTCTGAGATGTTGAAGTTCAGATGAGGAAAGAGCAGATTTGGGGTAAATCAAGGATCTGCATTG	3000
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Qy	3481	ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAAATCATGAGTATTTGGAAATAGAT	3540
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Qy	3601	ACCAGAGCTGTCTATATGGAAGAAAGACAGGACTGCAACTCAACCTTCAAAAATGAGGA	3660
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VERSION AR036572.1 GI:5953240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 246240)
AUTHORS Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
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QY	721	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACCTGG	780	QY	1801	GATGACAAATAGCAAAATGAGCAGAAAGATATACAAATCAGGAATCATGGGTGTTTGA	1860
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Db	193144	AAAGTTCTTCCCTGAGTGTTCGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	193203	Db	194224	AATAAGAAATGATATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	194283
QY	901	GGTTTCCACTCAGAACGAATCGTGTGGCGGTGGGGCGGAAAGAGTGCGGTTGGGA	960	QY	1981	TTGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGG	2040
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QY	961	TCGTGAATTTTCCACCATTTCCACCTTTTGGTGAGACTGGGTTGAGGCTCTAGGTT	1020	QY	2041	CGGGCTGGGGTGGGAAGGGGAGCTTACCATCTGCATGTAGATGTCTAGCAGTATCTGT	2100
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QY	1021	GGGAGGCTCCTGAGAGAGCCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080	QY	2101	CCTCCCTACTCACTAGTGTCTAGGAGCACTCCCCAGTCTTTGACAAACCAAAATGCTCT	2160
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QY	1321	GGAAATTCAGATTAATACTTTTTCAGGTTTACAAAGACATAAATAATCTGGTTTTCTG	1380	QY	2401	AAGGAGCAACAAGTAAAGAGCAGGAGCCAGCCAGGAAGCTGTTTACACAGTCCAGGCAAG	2460
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QY	1381	ATGTTATTTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTTGAAGTGAATTTTCCCTGTAG	1440	QY	2461	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGAGTGAACAAACCAATTTCTCCTGAA	2520
Db	193684	ATGTTATTTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTTGAAGTGAATTTTCCCTGTAG	193743	Db	194764	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGAGTGAACAAACCAATTTCTCCTGAA	194823
QY	1441	TGTAGCACAGTGTCTGTGGGTACACCGCCGCTCAGCACAGCACTTTGAGTTTGGTA	1500	QY	2521	TATATTTCTAGGAGGTTGCTGAGGATTTCTATGTTGTGTGAGGAGGAGGAGGATTTGG	2580
Db	193744	TGTAGCACAGTGTCTGTGGGTACACCGCCGCTCAGCACAGCACTTTGAGTTTGGTA	193803	Db	194824	TATATTTCTAGGAGGTTGCTGAGGATTTCTATGTTGTGTGAGGAGGAGGAGGATTTGG	194883
				QY	2581	CTGGGTGTAGTGTCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTTCTTGAGCTCAGGA	2640

Db	194884	CTGGGTGATAGTCTATCCCAAGGAGGAGGCGCAAGGAGAGCAGATTTCTGAGCTCAGGA	194943
Qy	2641	GTTCAGACAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAATATACAAAATTA	2700
Db	194944	GTTCAGACAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAATATACAAAATTA	195003
Qy	2701	GCTGGGTGGTGGCATGCACTGTGATCCTAGTACTCTCGGAGGCTGAGGTGGAGGTA	2760
Db	195004	GCTGGGTGGTGGCATGCACTGTGATCCTAGTACTCTCGGAGGCTGAGGTGGAGGTA	195063
Qy	2761	TTGCTTGAGCCAGGAGTTGAGGCTGAGTGCAGTGCATGCTGCCACTGTACTTTCAGC	2820
Db	195064	TTGCTTGAGCCAGGAGTTGAGGCTGAGTGCAGTGCATGCTGCCACTGTACTTTCAGC	195123
Qy	2821	CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT	2880
Db	195124	CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT	195183
Qy	2881	TCACCTTTGTTCTTTATTTTAAATTTTATTTGCTGAGCAGTGGGTAATTTGCCATGCCAT	2940
Db	195184	TCACCTTTGTTCTTTATTTTAAATTTTATTTGCTGAGCAGTGGGTAATTTGCCATGCCAT	195243
Qy	2941	TTCTGAGATGGTGAAGGACAGAAAGACAGCTTTGGGGTAATCAAGGATCTGATTTG	3000
Db	195244	TTCTGAGATGGTGAAGGACAGAAAGACAGCTTTGGGGTAATCAAGGATCTGATTTG	195303
Qy	3001	GGACATGTTAAGTTTGAGATTCAGTCCAGTCCAGCTTCAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	195304	GGACATGTTAAGTTTGAGATTCAGTCCAGTCCAGCTTCAAGTGGTGAGGCCACATAGGCAGTT	195363
Qy	3061	CAGTGTAGAAATTCAGGACCAAGGCTGGGACGCTGGCTCACTTCTGTAATCCAGCACT	3120
Db	195364	CAGTGTAGAAATTCAGGACCAAGGCTGGGACGCTGGCTCACTTCTGTAATCCAGCACT	195423
Qy	3121	TTGGTGGCTGAGGACAGTATGATTTGAGGTTCAGAGTTTGAGACAGCTTGGCCCAACA	3180
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Qy	3181	TGGTGAAACCCCATGTCTACTAAAAATACAAAAATAGCCCTGGTGGTGCGCAGCCT	3240
Db	195484	TGGTGAAACCCCATGTCTACTAAAAATACAAAAATAGCCCTGGTGGTGCGCAGCCT	195543
Qy	3241	ATAGTCCAGGTTTTCAGGAGCTTAGGTAGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	3300
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Qy	3301	TTGAGTGCAGTGCAGATTTGTCACCTGACCTGAGCTGGGTGATAGAGTGCATCTGT	3360
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Qy	3421	TCTAATTTTCCCTGAGCACAACCTCCTGAGTTCAACTACCTGCTGAGACACACCTTAAC	3480
Db	195724	TCTAATTTTCCCTGAGCACAACCTCCTGAGTTCAACTACCTGCTGAGACACACCTTAAC	195783
Qy	3481	ATTTTCTAGAAATCCACAGCTTTAGTGAGTCTGTCTAATCATGATGATTTGAAATAGGAT	3540
Db	195784	ATTTTCTAGAAATCCACAGCTTTAGTGAGTCTGTCTAATCATGATGATTTGAAATAGGAT	195843
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Db	195844	CTGGGGGAGTGCAGGGGGTGGCAGCCAGCTGGGAGGAGAAAGACACACAGGAAAGAGC	195903
Qy	3601	ACCCAGGACTGTCTATATGAGAGAGAGACAGGACTGCAACTCACCTTTCACAAAATGAGGA	3660
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Db	195964	CCAGACACAGCTGATGGTATGATGTCAGGTTGTGGAGCCTCAACATCCTGCTCCC	196023
Qy	3721	CTCCTACTACACATGTTAAGCCCTGTTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA	3780
Db	196024	CTCCTACTACACATGTTAAGCCCTGTTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA	196083
Qy	3781	CCTCTTCATGGTGGCTCAGAGCAGGACCTTGGTCTTTCTTGTGTTGAAAGCTTTGGGCTA	3840
Db	196084	CCTCTTCATGGTGGCTCAGAGCAGGACCTTGGTCTTTCTTGTGTTGAAAGCTTTGGGCTA	196143
Qy	3841	CCTGATGACCAAGCTGTTCTGTTCTATGATCATGAGTCCGCGTGTGGAGCCCCGAAC	3900
Db	196144	CCTGATGACCAAGCTGTTCTGTTCTATGATCATGAGTCCGCGTGTGGAGCCCCGAAC	196203
Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGAGCTGAGTCAGAGTCTGAA	3960
Db	196204	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGAGCTGAGTCAGAGTCTGAA	196263
Qy	3961	AGGTTGGATCAATGTTTCACTGTTGACTTTGGACTATTTATGGAANAATCAACAACACAG	4020
Db	196264	AGGTTGGATCAATGTTTCACTGTTGACTTTGGACTATTTATGGAANAATCAACAACACAG	196323
Qy	4021	CAAGGTTATGAGAGAGGGGCTCACCTTCTGAGGTTGTCAGAGCTTTTTCATCTTTTC	4080
Db	196324	CAAGGTTATGAGAGAGGGGCTCACCTTCTGAGGTTGTCAGAGCTTTTTCATCTTTTC	196383
Qy	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTTCTTGTGGAGCAGGAGAGGGAAG	4140
Db	196384	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTTCTTGTGGAGCAGGAGAGGGAAG	196443
Qy	4141	GAAATTTGCTTCTGAGATCATTTGCTTCTGAGGTTGTTGGAANAATGAGGACCTTATCTTT	4200
Db	196444	GAAATTTGCTTCTGAGATCATTTGCTTCTGAGGTTGTTGGAANAATGAGGACCTTATCTTT	196503
Qy	4201	TGGTTGAGTTTAAAGGCTGGGATTTTTCAGAGTCCCAACCTGAGAGTCACTCTG	4260
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Db	196564	GGCTGTGAAATGCAAGAGAGACAAAGTACCGAGGCTACTGGAAGTACGGGTATGATGG	196623
Qy	4321	CAGGACCACTTGAATTTGCTGCTGACACACTGGAATGGAAGCAGCAGAACCCAGGGCC	4380
Db	196624	CAGGACCACTTGAATTTGCTGCTGACACACTGGAATGGAAGCAGCAGAACCCAGGGCC	196683
Qy	4381	TGGCCCAACAGCTGGAGTGGGAAAGGACAAAGATTCGGGCGAGCAGACAGAGGCTTAC	4440
Db	196684	TGGCCCAACAGCTGGAGTGGGAAAGGACAAAGATTCGGGCGAGCAGACAGAGGCTTAC	196743
Qy	4441	CTGGAGAGGGACTGCGCTGACAGCTGAGCAGTTCCTGAGCTGGGAGAGGTGTTTTG	4500
Db	196744	CTGGAGAGGGACTGCGCTGACAGCTGAGCAGTTCCTGAGCTGGGAGAGGTGTTTTG	196803
Qy	4501	GACCAACAAGGTATGTTGGGAAACACACTTCTGCCCCCTATCTCTAGTGGCAGAGTGGAGG	4560
Db	196804	GACCAACAAGGTATGTTGGGAAACACACTTCTGCCCCCTATCTCTAGTGGCAGAGTGGAGG	196863
Qy	4561	AGGTTGAGGCGCAGGAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTGCTC	4620
Db	196864	AGGTTGAGGCGCAGGAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTGCTC	196923
Qy	4621	TCCAAATTTCTGGAGGGGACTTCTCAATCTAGAGTCTTACCTTATATTTAGATGTA	4680
Db	196924	TCCAAATTTCTGGAGGGGACTTCTCAATCTAGAGTCTTACCTTATATTTAGATGTA	196983
Qy	4681	TGAGACGCCACAAGTCAATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAGAGGAA	4740
Db	196984	TGAGACGCCACAAGTCAATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAGAGGAA	197043
Qy	4741	GTGCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTGTAA	4800
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QY	4801	AAATTCAGAAATGTC	AAAGCCGGGAC	CGGTGGCTCAC	CCCTGTAAATCC	AGCACTTTGGG	4860
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QY	4861	AGGCCGAGCGGGTGGT	CACAAGGTC	CAGGAGTTT	CAGACCAAGCTTG	ACCAATGGTGAA	4920
Db	197164	AGGCCGAGCGGGTGGT	CACAAGGTC	CAGGAGTTT	CAGACCAAGCTTG	ACCAATGGTGAA	197223
QY	4921	ACCCGCTCTCT	AAAAAATAC	AAAAATAGCTGGT	CACAGTCATGCG	CACCTGTAGTCCCA	4980
Db	197224	ACCCGCTCTCT	AAAAAATAC	AAAAATAGCTGGT	CACAGTCATGCG	CACCTGTAGTCCCA	197283
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QY	61	AATATCTAAAGTTCAGATCAGAACATTCGAAAGCTACTTTCCCAATCAACAAACCCCT	120				
Db	192364	AATATCTAAAGTTCAGATCAGAACATTCGAAAGCTACTTTCCCAATCAACAAACCCCT	192423				
QY	121	TCAGGATTTAAACCAAGGGGACACTGGATCACCTAGTGTTCACAAAGCAGGTACCTT	180				
Db	192424	TCAGGATTTAAACCAAGGGGACACTGGATCACCTAGTGTTCACAAAGCAGGTACCTT	192483				
QY	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAACCTGTGTCTTTTCAACGAAAGTT	240				
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QY	241	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG	300				
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QY	301	TTTCCCGCCGCCCAAGAGCGGAGATTTAAACGGGACGTCGCGGCAGAGCTGGGAA	360				
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QY	361	ATGGGCCCGCGAGCCAGGCCGCGCTCTCTCTGATGCTTTTTCAGACCGCGTCTG	420				
Db	192664	ATGGGCCCGCGAGCCAGGCCGCGCTCTCTCTGATGCTTTTTCAGACCGCGTCTG	192723				
QY	421	CAGGGCGCTTGCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG	480				

QY	1561	CAAAATTTATTCATAGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620	QY	2641	GTTCAAGACACAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
DB	193864	CAAAATTTATTCATAGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	193923	DB	194944	GTTCAAGACACAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	195003
QY	1621	TATGATTTCTTAACATCACATGCTATAGAGTTGAATTAATAAATTTTCATGTTAGCAG	1680	QY	2701	GCTGGGTGGTGGCATGCACTGTGATCTCTAGCTACTCGGAGGCTGAGGTGGAGGTA	2760
DB	193924	TATGATTTCTTAACATCACATGCTATAGAGTTGAATTAATAAATTTTCATGTTAGCAG	193983	DB	195004	GCTGGGTGGTGGCATGCACTGTGATCTCTAGCTACTCGGAGGCTGAGGTGGAGGTA	195063
QY	1681	AAATATTTCATTTTAAACAGTGAATAGTCCAGCCATGTGTGCACTGTTCAAGCCC	1740	QY	2761	TTGCTTTGAGCCAGCAAGTTGAGGCTGCACTGAGCCATGCTGTGCACTGTACTTTCAGC	2820
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DB	194044	CAAGGAGAGAGCAGGGAAACAAAGTCTTTACCTTTGATTAATTTGCAATCTAGTGGGAGA	194103	DB	195124	CTAGTGTGACAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTAAAGT	195183
QY	1801	GATGCAATTAAGCAATGACAGAAAGATATACATCAGGAATCATGGGTGTGTGA	1860	QY	2881	TGACCTTTGTTCTTTATTTTAAATTTTATTTGGCCCTGAGCAGTGGGTAAATTTGGCAATGCCAT	2940
DB	194104	GATGCAATTAAGCAATGACAGAAAGATATACATCAGGAATCATGGGTGTGTGA	194163	DB	195184	TGACCTTTGTTCTTTATTTTAAATTTTATTTGGCCCTGAGCAGTGGGTAAATTTGGCAATGCCAT	195243
QY	1861	GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTTGAGCAGAGACATGAAGGA	1920	QY	2941	TTCTCAGATGGTGAAGGAGAGAGAGAGAGTGGGTAAATCAAGGATCTGCAATTTG	3000
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QY	1921	ATAAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	1980	QY	3001	GGACATGTTAAGTTTGAGATTCCAGTCAAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
DB	194224	ATAAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	194283	DB	195304	GGACATGTTAAGTTTGAGATTCCAGTCAAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	195363
QY	1981	TTGGATTAAGAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	2040	QY	3061	CAGTGTAAAGATTCAGGACCAAGGCTGGGACGGTGGCTCACTTCTGTAAATCCAGCACT	3120
DB	194284	TTGGATTAAGAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	194343	DB	195364	CAGTGTAAAGATTCAGGACCAAGGCTGGGACGGTGGCTCACTTCTGTAAATCCAGCACT	195423
QY	2041	CGGCGTGGGGGTGGGAAGGGGACATACCATCTGATGTAGGATGCTAGCAGTATCTGT	2100	QY	3121	TTGGTGGCTGAGGAGGAGTAGATCATTTGAGGTCAGAGTTTCAGACAAGCTTTGGCCAAACA	3180
DB	194344	CGGCGTGGGGGTGGGAAGGGGACATACCATCTGATGTAGGATGCTAGCAGTATCTGT	194403	DB	195424	TTGGTGGCTGAGGAGGAGTAGATCATTTGAGGTCAGAGTTTCAGACAAGCTTTGGCCAAACA	195483
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DB	194404	CCTCCCTACTCACTAGGTCTAGGAGCACTCCCCCAGTCTTGACAAACCAAAATGTCTCT	194463	DB	195484	TGGTGAACCCCATGTCTACTAAAAAATACAAAAATACAAAAATACAAAAATACAAAAAT	195543
QY	2161	AAACTTTGGCAGATGCTACCTAGTACAGAACTCTCTGGTTTGAAGAGCTCGGGTTGAAAAA	2220	QY	3241	ATAGTCCAGGTTTTCAGGAGGCTTTAGGTAGGAGAAATCCCTTTGAACCCAGAGAGTGCAGG	3300
DB	194464	AAACTTTGGCAGATGCTACCTAGTACAGAACTCTCTGGTTTGAAGAGCTCGGGTTGAAAAA	194523	DB	195544	ATAGTCCAGGTTTTCAGGAGGCTTTAGGTAGGAGAAATCCCTTTGAACCCAGAGAGTGCAGG	195603
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DB	194524	ATAAACAAGTAGTGTGGGAGTAGAGCCCAAGAGTAGTAATGGGCTCAGAGAGGA	194583	DB	195604	TTGCACTGAGCTGAGATTGTCCACTCCAGCTCGGGTGTAGAGTAGAGTCTCTCT	195663
QY	2281	GCCCAAAACAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAGGAGTA	2340	QY	3361	CTCAAAAAAAGGTTTCAAAAAAAGGTTTCAAAAAAAGGTTTCAAAAAAAGGTTTCAAAAAA	3420
DB	194584	GCCCAAAACAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAGGAGTA	194643	DB	195664	CTCAAAAAAAGGTTTCAAAAAAAGGTTTCAAAAAAAGGTTTCAAAAAAAGGTTTCAAAAAA	195723
QY	2341	ACAGTGTATGTACAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAAGAGAGATG	2400	QY	3421	TCTAATTTGCCCTGAGGACCAACTCCTGAGTTCAACTACCTAGGCTAGACACACCTTAAAC	3480
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QY	2401	GAAGGAGCAACAGTAAAGAGGAGCCAGCAGGAGCTGTTACAGTCCAGGCAAG	2460	QY	3481	ATTTTCTAGAAATCCACAGCTTTTCTAGTGTCTGTCTAATCATGAGTATTTGCAATAGGAT	3540
DB	194704	GAAGGAGCAACAGTAAAGAGGAGCCAGCAGGAGCTGTTACAGTCCAGGCAAG	194763	DB	195784	ATTTTCTAGAAATCCACAGCTTTTCTAGTGTCTGTCTAATCATGAGTATTTGCAATAGGAT	195843
QY	2461	AGGTAGTGGAGTGGGTGGGAAACAGAAAGGGAGTGAACAAACCAATTTGCTCCTGAA	2520	QY	3541	CTGGGGGAGTGGGGGTGGGAGCCAGCTGTGGCAGAGAAAGCACAACAGGAAAGAGC	3600
DB	194764	AGGTAGTGGAGTGGGTGGGAAACAGAAAGGGAGTGAACAAACCAATTTGCTCCTGAA	194823	DB	195844	CTGGGGGAGTGGGGGTGGGAGCCAGCTGTGGCAGAGAAAGCACAACAGGAAAGAGC	195903
QY	2521	TATATTCTGAAGGAATGCTCTGAAGATTTCTATTTGTGTGAGAGAAAGAGAAATTTGG	2580	QY	3601	ACCCAGGACTGTATATGGAAAGAAAGAGAGGAGTCAACTCCTTTCACAAAAATGAGGA	3660
DB	194824	TATATTCTGAAGGAATGCTCTGAAGATTTCTATTTGTGTGAGAGAAAGAGAAATTTGG	194883	DB	195904	ACCCAGGACTGTATATGGAAAGAAAGAGAGGAGTCAACTCCTTTCACAAAAATGAGGA	195963
QY	2581	CTGGGTGTAGTACTCATGCCAAGGAGGAGGCAAGGAGGAGCAGATTCTGAGCTCAGGA	2640	QY	3661	CCAGACACAGCTGTATGTTGATGTTGATGTTGAGGAGCTTCAACATCTCTCTCTCC	3720
DB	194884	CTGGGTGTAGTACTCATGCCAAGGAGGAGGCAAGGAGGAGCAGATTCTGAGCTCAGGA	194943	DB	195964	CCAGACACAGCTGTATGTTGATGTTGATGTTGAGGAGCTTCAACATCTCTCTCTCC	196023
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VERSION AR036574.1 GI:5953242
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REFERENCE 1 (bases 1 to 246240)
AUTHORS Feder,J.,Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Thomas,W., Teuchihashi,Z. and Wolff,R.K.
TITLE Megabase transcript map: novel sequences and antibodies thereto
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REFERENCE 1 (bases 1 to 10825)
AUTHORS Unclassified.
Thomas, W. J., Drayna, D. T., Feder, J. N., Gnirke, A., Ruddy, D.,
Tsuchinashi, Z., and Wolff, R. K.
TITLE Hereditary hemochromatosis gene products
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DEFINITION Sequence 7 from patent US 6140305.
ACCESSION AR117792
VERSION AR117792.1 GI:14098698
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas W.J., Drayna D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolf, R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 7 31-OCT-2000;
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DEFINITION Sequence 5 from patent US 6228594.
ACCESSION ARI149461
VERSION ARI149461.1 GI:151114052
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Teuchihashi, Z. and Wolff, R. K.
TITLE Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
JOURNAL Patent: US 6228594-A 5 08-MAY-2001;
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LOCUS AR149462 10825 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6228594.
ACCESSION AR149462
VERSION AR149462.1 GI:15114053
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
JOURNAL Patent: US 6228594-A 7 08-MAY-2001;
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SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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CDS	complement(16434. .16826) /codon_start=1 /product="histone 2A-like protein"		/protein_id="AAB82083.1" /db_xref="GI:2088551"
	complement(18988. .19282) /rpt_family="Alu" /rpt_type=dispersed	repeat_region	/translation="MGPRARPALLMLLQTAVLQGRLLRSHSLHYLPMGASEQDLGL SLPEALGYDDQDFVFDHESRRVEPTPWSSRISQMWLQLSKLGWDMFTVDF WTIMENHNKESHKTRLOVILGCENQEDNSTEGYKYGVDGQDHLFCFDDTLDMRAAEP RAWPTKWEKHKIRARONRAYLERDCPAQQLLELGRVLDQVPLVKVTHHTVS SVTTLRCRALNYYPQNTMKWLKDKQPMDAKEPEKDVLPNGDGTQYQSMITLAVPGE SQRTQVEHPGLDQPLIVIEWPSGTLVIGVISGIAVFWILFIGILFILLRKQGS BQGWAGHYVLARE"
repeat_region	complement(20597. .20869) /rpt_family="Alu" /rpt_type=dispersed		complement(48868. .49182) /rpt_family="Alu" /rpt_type=dispersed
repeat_region	complement(24343. .24624) /rpt_family="Alu" /rpt_type=dispersed	repeat_region	complement(50599. .50888) /rpt_family="Alu" /rpt_type=dispersed
repeat_region	25654. .25805 /rpt_family="MIR" /rpt_type=dispersed	repeat_region	complement(51145. .51372) /rpt_family="Alu" /rpt_type=dispersed
repeat_region	29842. .29938 /rpt_family="Alu" /rpt_type=dispersed	repeat_region	51820. .51934 /rpt_family="MER20" /rpt_type=dispersed
repeat_region	complement(30592. .30869) /rpt_family="Alu" /rpt_type=dispersed	repeat_region	55276. .55719 /rpt_family="Alu" /rpt_type=dispersed
repeat_region	31223. .31507 /rpt_family="Alu" /rpt_type=dispersed	repeat_region	complement(56085. .56461) /rpt_family="L1" /rpt_type=dispersed
repeat_region	complement(31819. .32011) /rpt_family="Alu" /rpt_type=dispersed	repeat_region	complement(56521. .56801) /rpt_family="Alu" /rpt_type=dispersed
repeat_region	33810. .34150 /rpt_family="MER1" /rpt_type=dispersed	repeat_region	57660. .57815 /rpt_family="Alu" /rpt_type=dispersed
repeat_region	34235. .34314 /rpt_family="Alu" /rpt_type=dispersed	repeat_region	58118. .58483 /rpt_family="MLT1" /rpt_type=dispersed
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repeat_region	complement(36267. .36548) /rpt_family="Alu" /rpt_type=dispersed	repeat_region	complement(59299. .59737) /rpt_family="LTR2" /rpt_type=dispersed
repeat_region	39132. .39252 /rpt_family="Alu" /rpt_type=dispersed	repeat_region	complement(65665. .66013) /rpt_family="LTR2" /rpt_type=dispersed
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Query Match	99.8%; Score 4988; DB 9; Length 246282;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 4999; Conservative	0; Mismatches	0; Indels 1; Gaps 1;
QY 1	TCTAAGGTTTCAGATATAAATTTTAAATGTATGATGAATTTTCAAAATCATAAATATTTA 60	52958 GGGAGGCTCCTGAGAGAGCCCTACCTCGGGCCCTTTCCCACTCTTGCAATTTCTTTT 52899
DB 53978	TCTAAGGTTGAGATATAAATTTTAAATGTATGATGAATTTTCAAAATCATAAATATTTA 53919	1081 GCGTGAATAATTAAGTATATGTAGTTTGAAGCTTTGAACAAATCTCTTTTCGG 1140
QY 61	AATATCTAAAGTTTCAGATCAGAAATTTGCGAAGCTACTTTTCCCAATCAACACACCCCT 120	52898 GCGTGAATAATTAAGTATATGTAGTTTGAAGCTTTGAACAAATCTCTTTTCGG 52839
DB 53918	AATATCTAAAGTTTCAGATCAGAAATTTGCGAAGCTACTTTTCCCAATCAACACACCCCT 53859	1141 CTAGGCTTTATGATTTGCAATGTCTGTGTAAATTAAGAGGCCCTCTCTACAAAGTACTGA 1200
QY 121	TCAGGATTTAAACCAAGGGGACACTGATCACCCTAGTGTTCACAGAGGATACCTT 180	52838 CTAGGCTTTATGATTTGCAATGTCTGTGTAAATTAAGAGGCCCTCTCTACAAAGTACTGA 52779
DB 53858	TCAGGATTTAAACCAAGGGGACACTGATCACCCTAGTGTTCACAGAGGATACCTT 53799	1201 TAATGAACATGTAAAGCAATGCACTCACTTCTAAGTTTACATTTTCATATCTGATCTTATTTGA 1260
QY 181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGTAAGACCTGTGTCTTTTCAACAGGAGTT 240	52778 TAATGAACATGTAAAGCAATGCACTCACTTCTAAGTTTACATTTTCATATCTGATCTTATTTGA 52719
DB 53798	CTGCTGTAGGAGAGAGAACTAAAGTTCTGTAAGACCTGTGTCTTTTCAACAGGAGTT 53739	1261 TTTTTCATAGGCATAGGAGGAGGAGGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320
QY 241	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 300	52718 TTTTTCATAGGCATAGGAGGAGGAGGCTAAATAACGTTTATTTTACTAGAGTTAACT 52659
DB 53738	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 53679	1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTTCAAGAAACATAAATAAATCTGTTTCTG 1380
QY 301	TTTCCCGCCGCCCAAAAGCGGAGATTTAAACGGGACGTCGCGGCCAGAGCTGGGAA 360	52658 GGAATTCAGATTAATAAATCTTTTTCAGGTTTCAAGAAACATAAATAAATCTGTTTCTG 52599
DB 53678	TTTCCCGCCGCCCAAAAGCGGAGATTTAAACGGGACGTCGCGGCCAGAGCTGGGAA 53619	1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTCTAAGTTTGAAGTATTTGCCCCGTGAG 1440
QY 361	ATGGGCGCGGAGCGGCGGCTTCTCTCTGATGCTTTTGAGACCGCGGTCTG 420	52598 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTCTAAGTTTGAAGTATTTGCCCCGTGAG 52539
DB 53618	ATGGGCGCGGAGCGGCGGCTTCTCTCTGATGCTTTTGAGACCGCGGTCTG 53559	1441 TCTAGCAGAGCTGCTTCTGCGGTCACGCGCGGCTTCAGCAGCAGCTTTGAGTTTGGTA 1500
QY 421	CAGGGCGCTTGTGCGTGAAGTCCGAGGCTGCGGCGGAACTAGGGCGCGCGGGGTG 480	52538 TGTAGCAGAGCTTCTGCGGTCACGCGCGGCTTCAGCAGCAGCTTTGAGTTTGGTA 52479
DB 53558	CAGGGCGCTTGTGCGTGAAGTCCGAGGCTGCGGCGGAACTAGGGCGCGCGGGGTG 53499	1501 CTACGCTGATCCACATTTTACATGACAAGATGAGGCTGCGCAGGCTGCTTCTCTG 1560
QY 481	GAAAAATCGAACTAGCTTTTCTTTCGCTTGGGAGTTTGTAACTTTGGAGGACCTGC 540	52478 CTACGCTGATCCACATTTTACATGACAAGATGAGGCTGCGCAGGCTGCTTCTCTG 52419
DB 53498	GAAAAATCGAACTAGCTTTTCTTTCGCTTGGGAGTTTGTAACTTTGGAGGACCTGC 53439	1561 CAAATTTATTCATTTCAAGTAAATGAGTCCAGCCATGTTGTGCACTGTTTCAAGCCC 1740
QY 541	TCACCCCTATCCGAGCCCTCTCCCTACTTTTCTGCTTCCAGCCCGCTGAGGAGTGC 600	52418 CAAATTTATTCATTTCAAGTAAATGAGTCCAGCCATGTTGTGCACTGTTTCAAGCCC 52359
DB 53438	TCACCCCTATCCGAGCCCTCTCCCTACTTTTCTGCTTCCAGCCCGCTGAGGAGTGC 53379	1621 FATGATTTTAAACATCACTGCACTTAAAGTTCGAATTAATAAATTTTCACTGTTGAGCAG 1680
QY 601	CTACCACTGAACTGAGATAGGGTCCCTCGCCCCAGAGACCTGCCCCCTCCCGGCTGT 660	52358 FATGATTTTAAACATCACTGCACTTAAAGTTCGAATTAATAAATTTTCACTGTTGAGCAG 52299
DB 53378	CTACCACTGAACTGAGATAGGGTCCCTCGCCCCAGAGACCTGCCCCCTCCCGGCTGT 53319	1681 AAATTTTATTCATTTTCAAGTAAATGAGTCCAGCCATGTTGTGCACTGTTTCAAGCCC 1740
QY 661	CCGGCTCTGCGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAAATGCTTT 720	52298 AAATTTTATTCATTTTCAAGTAAATGAGTCCAGCCATGTTGTGCACTGTTTCAAGCCC 52239
DB 53318	CCGGCTCTGCGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAAATGCTTT 53259	1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGGAGA 1800
QY 721	TAAATAAATCTCGTAGTTCCTCACTGAGCTGAGCTTAAGCTTGGGCTCTTTGAACCTGG 780	52238 CAAGGAGAGAGCAGGGAACAAAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGGAGA 52179
DB 53258	TAAATAAATCTCGTAGTTCCTCACTGAGCTGAGCTTAAGCTTGGGCTCTTTGAACCTGG 53199	1801 GATGCAATTAAGCAATGAGCAGAAAGATATACACATCAGGAATCATGGGTGTTGTA 1860
QY 781	AACTCGGGTTATTTTCCAATGTCACTGTGCAAGTTTTCCTCCAGTCACTCCAAACAGG 840	52178 GATGCAATTAAGCAATGAGCAGAAAGATATACACATCAGGAATCATGGGTGTTGTA 52119
DB 53198	AACTCGGGTTATTTTCCAATGTCACTGTGCAAGTTTTCCTCCAGTCACTCCAAACAGG 53139	1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGGAGCAGACATGAAGA 1920
QY 841	AAAGTTCTCCCTGAGTGTTCGCGAAGGCTGAGCAACCCACAGCAGGATCCGACCG 900	52118 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGGAGCAGACATGAAGA 52059
DB 53138	AAAGTTCTCCCTGAGTGTTCGCGAAGGCTGAGCAACCCACAGCAGGATCCGACCG 53079	1921 AATAAATATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTCAGTGGGCTTGGCAAG 1980
QY 901	GGTTTCCACTCAGAACGAATGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTGGGA 960	52058 AATAAATATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTCAGTGGGCTTGGCAAG 51999
DB 53078	GGTTTCCACTCAGAACGAATGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTGGGA 53019	1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
QY 961	TTCTGAATTTCTCAACCACTTTTGTGTGAGACCTGCGGCTGAGGCTCTTAGGGT 1020	51998 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 51939
DB 53018	TTCTGAATTTCTCAACCACTTTTGTGTGAGACCTGCGGCTGAGGCTCTTAGGGT 52959	2041 CGGCTGGGGTGGGAAGGGGACTTACCCTCTGCACTGAGGATGCTTAGCAGTATCTCTGT 2100
QY 1021	GGGAGGCTCCTGAGAGAGGCTACCTCGGGCCCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080	51938 CGGCTGGGGTGGGAAGGGGACTTACCCTCTGCACTGAGGATGCTTAGCAGTATCTCTGT 51879
DB 1080	GGGAGGCTCCTGAGAGAGGCTACCTCGGGCCCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080	2101 CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCGCAGTCTTGGACAAACCAAAATGCTCTCT 2160

Db	51878	CCTCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTTGACAAACAAATGCTCTCT	51819
Qy	2161	AAACTTTGCGCATGTGACCTAGTATAGACAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAAA	2220
Db	51818	AAACTTTGCGCATGTGACCTAGTATAGACAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAAA	51759
Qy	2221	AATAAACAGTAGTGTCTGGGAGTAGAGCCAAAGAGTAGGTAAATGGGCTCAGAGAGGA	2280
Db	51758	AATAAACAGTAGTGTCTGGGAGTAGAGCCAAAGAGTAGGTAAATGGGCTCAGAGAGGA	51699
Qy	2281	GCCACAAACAGGTTGTGCGAGCGCTGTAGGCTGTGGTGTGAAATTTAGCCCAAGAGTA	2340
Db	51698	GCCACAAACAGGTTGTGCGAGCGCTGTAGGCTGTGGTGTGAAATTTAGCCCAAGAGTA	51639
Qy	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTCTATGTGGAAAGAGATG	2400
Db	51638	ACAGTGATCTGTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTCTATGTGGAAAGAGATG	51579
Qy	2401	AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGGAGCTGTACAGATCCAGGCAAG	2460
Db	51578	AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGGAGCTGTACAGATCCAGGCAAG	51519
Qy	2461	AGGTAGTGGAGTGGCTGGGTCGGGAACAGAAAAGGAGTGACAAACCATTTGCTCCTGAA	2520
Db	51518	AGGTAGTGGAGTGGCTGGGTCGGGAACAGAAAAGGAGTGACAAACCATTTGCTCCTGAA	51459
Qy	2521	TATATTTGAAGGAATGCTGAAGGATTTCTATGTTGTGTGAGAAAGAGAAATTTGG	2580
Db	51458	TATATTTGAAGGAATGCTGAAGGATTTCTATGTTGTGTGAGAAAGAGAAATTTGG	51399
Qy	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGCCAAAGGAGCAGATTTCTGTAGCTCAGGA	2640
Db	51398	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGCCAAAGGAGCAGATTTCTGTAGCTCAGGA	51339
Qy	2641	GTTCAGACAGCCTCGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA	2700
Db	51338	GTTCAGACAGCCTCGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA	51279
Qy	2701	GCTGGGTGTGGCATGCACTGTGATCTGTAGCTACTCGGAGGCTGAGGTGAGGTA	2760
Db	51278	GCTGGGTGTGGCATGCACTGTGATCTGTAGCTACTCGGAGGCTGAGGTGAGGTA	51219
Qy	2761	TTGCTTGAGCCAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTGACTTACG	2820
Db	51218	TTGCTTGAGCCAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTGACTTACG	51159
Qy	2821	CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT	2880
Db	51158	CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT	51099
Qy	2881	TGACTTTGTTCTTTTATTTTATTTTATTTGGCTGAGCAGTGGGTTAATTTGGCAATGCCAT	2940
Db	51098	TGACTTTGTTCTTTTATTTTATTTTATTTGGCTGAGCAGTGGGTTAATTTGGCAATGCCAT	51039
Qy	2941	TTCTCAGATGTGTAAGGAGAGGAAGAGCAGTTTGGGTTAATCAAGATCTGCAATTTG	3000
Db	51038	TTCTCAGATGTGTAAGGAGAGGAAGAGCAGTTTGGGTTAATCAAGATCTGCAATTTT	50980
Qy	3001	GGACATGTTAAGTTTGTAGATTTCCAGTTCAGGCTTCCAAGTGTGTGAGGCCACATAGGCAT	3060
Db	50979	GGACATGTTAAGTTTGTAGATTTCCAGTTCAGGCTTCCAAGTGTGTGAGGCCACATAGGCAT	50920
Qy	3061	CAGTGTAAGAAATTCAGGACCAAGGCTGGGCAAGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Db	50919	CAGTGTAAGAAATTCAGGACCAAGGCTGGGCAAGGTGGCTCACTTCTGTAAATCCAGCACT	50860
Qy	3121	TTGTGGCTGAGCGAGGTAGATCATTTGAGGTTCAGAGTTTTCAGACAAAGCTTTGGCAACA	3180
Db	50859	TTGTGGCTGAGCGAGGTAGATCATTTGAGGTTCAGAGTTTTCAGACAAAGCTTTGGCAACA	50800
Qy	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGCGCACGCT	3240
Db	50799	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGCGCACGCT	50740
Qy	3241	ATAGTCCCAGGTTTTCAGAGGCTTAGGTAGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
Db	50739	ATAGTCCCAGGTTTTCAGAGGCTTAGGTAGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	50680
Qy	3301	TTGCACTGAGCTGAGATTTGTGCCACTGCCAGCTGGGTGTAGAGTGTAGATCTGT	3360
Db	50679	TTGCACTGAGCTGAGATTTGTGCCACTGCCAGCTGGGTGTAGAGTGTAGATCTGT	50620
Qy	3361	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	3420
Db	50619	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	50560
Qy	3421	TCTAATTTTCCCTTGAGCACTCCTCAGTTCACCTGAGTTCACCTGAGTTCACCTGAGT	3480
Db	50559	TCTAATTTTCCCTTGAGCACTCCTCAGTTCACCTGAGTTCACCTGAGTTCACCTGAGT	50500
Qy	3481	ATTTTCTAGAAATCCACAGCTTTTAGTGAGTCTGTCTAATCATGAGTATTTGAAATAGGAT	3540
Db	50499	ATTTTCTAGAAATCCACAGCTTTTAGTGAGTCTGTCTAATCATGAGTATTTGAAATAGGAT	50440
Qy	3541	CTGGGGCAGTGAAGGGTGGCAGCCAGTGTGGCAGAAAAAGCACAAAGGAAAGAGC	3600
Db	50439	CTGGGGCAGTGAAGGGTGGCAGCCAGTGTGGCAGAAAAAGCACAAAGGAAAGAGC	50380
Qy	3601	ACCCAGGACTGTCTATATGGAAGAAAGACAGACTGCAACTCACCTTCACAAAAATGAGA	3660
Db	50379	ACCCAGGACTGTCTATATGGAAGAAAGACAGACTGCAACTCACCTTCACAAAAATGAGA	50320
Qy	3661	CCAGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3720
Db	50319	CCAGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	50260
Qy	3721	CTCCTACTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3780
Db	50259	CTCCTACTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	50200
Qy	3781	CCTCTTCAATGGTGCCTCAGAGCAGGACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTT	3840
Db	50199	CCTCTTCAATGGTGCCTCAGAGCAGGACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTT	50140
Qy	3841	CGTGATGACAGCTGTTTCTGTTCTATGATCATGAGAGTGCCTGCTGGAGCCCGAAC	3900
Db	50139	CGTGATGACAGCTGTTTCTGTTCTATGATCATGAGAGTGCCTGCTGGAGCCCGAAC	50080
Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGCGCTGAGTGTGAGTGTGAGTGT	3960
Db	50079	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGCGCTGAGTGTGAGTGTGAGTGT	50020
Qy	3961	AGGTTGGGATCAGATGTTTCTGTTGACTTCTGGAATTTATGGAATTTATGGAATTTAT	4020
Db	50019	AGGTTGGGATCAGATGTTTCTGTTGACTTCTGGAATTTATGGAATTTATGGAATTTAT	49960
Qy	4021	CAAGGTTATGTTGAGAGGGGCTCACCTTCTCAGAGTTGTGAGAGCTTTTTCATCTTTTC	4080
Db	49959	CAAGGTTATGTTGAGAGGGGCTCACCTTCTCAGAGTTGTGAGAGCTTTTTCATCTTTTC	49900
Qy	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTTTGTGGGAGCAGGGAAGAGGAG	4140
Db	49899	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTTTGTGGGAGCAGGGAAGAGGAG	49840
Qy	4141	GAAATTTGCTTCTCAGATCATTTGGTCTTGGGATGTTGGAATTTAGGAGCTATTTCTT	4200
Db	49839	GAAATTTGCTTCTCAGATCATTTGGTCTTGGGATGTTGGAATTTAGGAGCTATTTCTT	49780
Qy	4201	TGGTTGAGTTAAACAGGCTGGGATTTTTCAGAGTCCCAACACCTTCAGGCTATCTCTG	4260
Db	49779	TGGTTGAGTTAAACAGGCTGGGATTTTTCAGAGTCCCAACACCTTCAGGCTATCTCTG	49720
Qy	4261	GGCTGTGAAATGCAAGAAAGACAAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGG	4320
Db	49719	GGCTGTGAAATGCAAGAAAGACAAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGG	49660

QY	841	AA	GTTCCTCTGAGTCTGTCGCCGAGAAGGCTGAGCAAAACCCACAGCAGAAATCCGACGG	900
DB	46261	AA	GTTCCTCTGAGTCTGTCGCCGAGAAGGCTGAGCAAAACCCACAGCAGAAATCCGACGG	46202
QY	901	GG	TTTCCACCTCAGAACGAATGGTTGGCGGTGGGGGCGCGAAGAGTGGGCTTGGGGA	960
DB	46201	GG	TTTCCACCTCAGAACGAATGGTTGGCGGTGGGGGCGCGAAGAGTGGGCTTGGGGA	46142
QY	961	TCT	GAAATTTCTTCAACATTTCCACCACTTTTGTGTGAGACCTGGGGGTGGAGGTCTCTAGAGT	1020
DB	46141	TCT	GAAATTTCTTCAACATTTCCACCACTTTTGTGTGAGACCTGGGGGTGGAGGTCTCTAGAGT	46082
QY	1021	GGG	AGGCTCTGTGAGAGAGGCTTACTCTGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080
DB	46081	GGG	AGGCTCTGTGAGAGAGGCTTACTCTGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	46022
QY	1081	GCCT	TGGAAATTAAGTATATATTTAGTTTGTGAAGCTTTGAACCTTGAACCAATTTCTTTTCGG	1140
DB	46021	GCCT	TGGAAATTAAGTATATATTTAGTTTGTGAAGCTTTGAACCTTGAACCAATTTCTTTTCGG	45962
QY	1141	CTAG	CTTTTATTTGATTTGGCAATGTGTGTAAATAAGAGGCTCTCTACAAAGTACTGA	1200
DB	45961	CTAG	CTTTTATTTGATTTGGCAATGTGTGTAAATAAGAGGCTCTCTACAAAGTACTGA	45902
QY	1201	TAAT	GAACTGTGAAGCAATGCACTCATCTTCTAAGTTTACAATTCATATCTGATCTTATTTGA	1260
DB	45901	TAAT	GAACTGTGAAGCAATGCACTCATCTTCTAAGTTTACAATTCATATCTGATCTTATTTGA	45842
QY	1261	TTTT	CACCTAGGCATAGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT	1320
DB	45841	TTTT	CACCTAGGCATAGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT	45782
QY	1321	GGAA	TTCCAGATTTATAAATCTTTTCCAGGTTACAAAGAAACATAAAATAATCTGTTTTCCTG	1380
DB	45781	GGAA	TTCCAGATTTATAAATCTTTTCCAGGTTACAAAGAAACATAAAATAATCTGTTTTCCTG	45722
QY	1381	ATGT	TATTTCAAGTACTAGAGTGTCTTAACTTTAGTTTGAAGTGAATTTGGCCCTGTAG	1440
DB	45721	ATGT	TATTTCAAGTACTAGAGTGTCTTAACTTTAGTTTGAAGTGAATTTGGCCCTGTAG	45662
QY	1441	TGT	AGCACAGTGTCTGTGGGTACACGCGCGGCTCCAGCACAGCACTTTTGAGTTTGTGA	1500
DB	45661	TGT	AGCACAGTGTCTGTGGGTACACGCGCGGCTCCAGCACAGCACTTTTGAGTTTGTGA	45602
QY	1501	CTAC	GTGTATCCACATTTTACATGACAAAGATAGGCGATGGCGCGCTGCTTCTCTGG	1560
DB	45601	CTAC	GTGTATCCACATTTTACATGACAAAGATAGGCGATGGCGCGCTGCTTCTCTGG	45542
QY	1561	CAAA	TTTTTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
DB	45541	CAAA	TTTTTCAATGTGTGTACCGGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	45482
QY	1621	TAT	GATTTCTTTAAACATCACACTGATTTAGAGTTTGAATAATAAAATTTTCATGTTGAGCAG	1680
DB	45481	TAT	GATTTCTTTAAACATCACACTGATTTAGAGTTTGAATAATAAAATTTTCATGTTGAGCAG	45422
QY	1681	AAAT	TATTCATTTGTTTTCAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC	1740
DB	45421	AAAT	TATTCATTTGTTTTCAAGTGTAAATGAGTCCCAGCCATGTGTTGCACTGTTCAAGCCC	45362
QY	1741	CAAG	GGAGAGCAGGGAAACAGTCTTTTACCTTTTGATATTTTGCATCTCTAGTGGGAGA	1800
DB	45361	CAAG	GGAGAGCAGGGAAACAGTCTTTTACCTTTTGATATTTTGCATCTCTAGTGGGAGA	45302
QY	1801	GAT	GACAAATAAGCAAAATGAGCAGAAAGATATACCAATCAGGAAATCATGGGTGTTTGA	1860
DB	45301	GAT	GACAAATAAGCAAAATGAGCAGAAAGATATACCAATCAGGAAATCATGGGTGTTTGA	45242
QY	1861	GAAG	CAGAGAAGTCTCAGGGCAAGTCACTCTGGGGCTGCACTTTGAGCAGACATGAAGGA	1920
DB	45241	GAAG	CAGAGAAGTCTCAGGGCAAGTCACTCTGGGGCTGCACTTTGAGCAGACATGAAGGA	45182

[illegible]

REFERENCE	1	(bases 1 to 12146)	
AUTHORS	Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.		
TITLE	Mutations associated with iron disorders		
JOURNAL	Patent: US 6355425-A 27 12-MAR-2002;		
FEATURES	Location/Qualifiers		
source	1..12146		
ORIGIN	/organism="unknown" /mol_type="unassigned DNA"		
Query Match	99.1%;	Score 4957.2;	DB 6; Length 12146;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 4995;	Conservative 0;	Mismatches 3;	Indels 6; Gaps 3;
Qy	1	TCTAAGGTTGAGATAAAATTTTTAAATGTATGATTGAATTTTGGAAAATCATAAATATTTA	60
Db	889	TCTAAGGTTGAGATAAAATTTTTAAATGTATGATTGAATTTTGGAAAATCATAAATATTTA	948
Qy	61	AATATCTAAAGTTCAGATCAGAACATTTCCGAAGTACTTTTCCCCAATCAAACACCCCT	120
Db	949	AATATCTAAAGTTCAGATCAGAACATTTCCGAAGTACTTTTCCCCAATCAAACACCCCT	1008
Qy	121	TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTTTTCACAGCAGGTACCTT	180
Db	1009	TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTTTTCACAGCAGGTACCTT	1068
Qy	181	CTGCTGTAGGAGAGAGAGAAGACTAAAGTTCTGAAAGACTGTGTGCTTTTACCACAGGAAGTT	240
Db	1069	CTGCTGTAGGAGAGAGAGAAGACTAAAGTTCTGAAAGACTGTGTGCTTTTACCACAGGAAGTT	1128
Qy	241	TTACTGGGCATCTCTCGAGCCTAGGCCAATAGCTGTAGGGTAGCTTCTGGAGCCATCCCCG	300
Db	1129	TTACTGGGCATCTCTCGAGCCTAGGCCAATAGCTGTAGGGTAGCTTCTGGAGCCATCCCCG	1188
Qy	301	TTTCCCGCCCCCAAAAGAGCGGAGATTTAAACGGGGAAGTGGCGGCACAGCTGGGGAA	360
Db	1189	TTTCCCGCCCCCAAAAGAGCGGAGATTTAAACGGGGAAGTGGCGGCACAGCTGGGGAA	1248
Qy	361	ATGGGCGCGGAGCAGCGCGGCGCTTCTCCTCTGATGCTTTTTCAGACCGCGGTCTTG	420
Db	1249	ATGGGCGCGGAGCAGCGCGGCGCTTCTCCTCTGATGCTTTTTCAGACCGCGGTCTTG	1308
Qy	421	CAGGGCGGCTTGCTGCGTGAAGTCCGAGGGCTGCGGGCGAACTAGGGCGCGGGGGGTG	480
Db	1309	CAGGGCGGCTTGCTGCGTGAAGTCCGAGGGCTGCGGGCGAACTAGGGCGCGGGGGGTG	1368
Qy	481	GAAAAATCGAAACTAGCTTTTCTTTGGGCTTGGGAGTTTGCTAACTTTGGAGAACCTGC	540
Db	1369	GAAAAATCGAAACTAGCTTTTCTTTGGGCTTGGGAGTTTGCTAACTTTGGAGAACCTGC	1428
Qy	541	TCAACCTATCCGACAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGGAGGAGTGC	600
Db	1429	TCAACCCAAATCCGACAGCCCTCTCCCTACTTTCTGGGTCCAGACCCCGTGGAGGAGTGC	1488
Qy	601	CTACCACTGAACTCAGATAGGGGTCTCTCGCCCCCAGGACCTGCGCCCTCTCCCCCGGCTGT	660
Db	1489	CTACCACTGAACTCAGATAGGGGTCTCTCGCCCCCAGGACCTGCGCCCTCTCCCCCGGCTGT	1548
Qy	661	CCCGGCTCTCGGAGTGACTTTTGGAAACCGGCCACTCCCTTCCCCCAACTAGAAATGCTTT	720
Db	1549	CCCGGCTCTCGGAGTGACTTTTGGAAACCGGCCACTCCCTTCCCCCAACTAGAAATGCTTT	1608
Qy	721	TAAATAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACTGCG	780
Db	1609	TAAATAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTGAACTGCG	1668
Qy	781	AACTCGGGTTTATTTCCAATGTGAGCTGTGAGTTTTTTTCCCAAGTCACTCTCCAAAACAGG	840
Db	1669	AACTCGGGTTTATTTCCAATGTGAGCTGTGAGTTTTTTTCCCAAGTCACTCTCCAAAACAGG	1728
Qy	841	AAGTTCCTCTCGAGTGCTTCCGAGAGGCTGAGCAAAACCAACAGCAGGATCCGCAAG	900
Db	1729	AAGTTCCTCTCGAGTGCTTCCGAGAGGCTGAGCAAAACCAACAGCAGGATCCGCAAG	1788

Db 5027 GAAGGAATTTGCTTCTGAGATCATTTGGTCTTGGGGATGGTGAATAAGGACCTATT 5086
QY 4197 CCTTTGGTTGCAGTTTAA CAAGGCTGGGATTTTTCCAGAGTCCACACCCCTGCAGGTCA 4256
Db 5087 CCTTTGGTTGCAGTTTAA CAAGGCTGGGATTTTTCCAGAGTCCACACCCCTGCAGGTCA 5146
QY 4257 CCTGGGCTGTGNAATGCAAGAGACAA CAGTACCGAGGGCTACTGGAAGTACGGGTATGA 4316
Db 5147 CCTGGGCTGTGNAATGCAAGAGACAA CAGTACCGAGGGCTACTGGAAGTACGGGTATGA 5206
QY 4317 TGGGCAGGACCACTTTGAAATCTGCCCTGCACACACTGGATTGGAGAGCAGACAGCCAG 4376
Db 5207 TGGGCAGGACCACTTTGAAATCTGCCCTGCACACACTGGATTGGAGAGCAGACAGCCAG 5266
QY 4377 GGCCTGGCCCCAACAAAGCTGGAGTGGGAAAGGCACAAAGATTGGGGCCAGGCAGAA CAGGGC 4436
Db 5267 GGCCTGGCCCCAACAAAGCTGGAGTGGGAAAGGCACAAAGATTGGGGCCAGGCAGAA CAGGGC 5326
QY 4437 CTACCTGAGAGGAGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGT 4496
Db 5327 CTACCTGAGAGGAGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGT 5386
QY 4497 TTTGACCAACAAAGTATGGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTG 4556
Db 5387 TTTGACCAACAAAGTATGGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTG 5446
QY 4557 GAGGAGTTGCAGGGCACCGAATCCCTGGTTGGAGTTT CAGAGSTGGCTGAGGCTGTGTG 4616
Db 5447 GAGGAGTTGCAGGGCACCGAATCCCTGGTTGGAGTTT CAGAGSTGGCTGAGGCTGTGTG 5506
QY 4617 CCTCTCCAAATCTGGGAGGAGCTTCTCAATCCTAGAGTCTCTACCTTATATTGAGA 4676
Db 5507 CCTCTCCAAATCTGGGAGGAGCTTCTCAATCCTAGAGTCTCTACCTTATATTGAGA 5566
QY 4677 TGTATGACAGCCACAAGTCATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAAG 4736
Db 5567 TGTATGACAGCCACAAGTCATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAAG 5626
QY 4737 GGAAGTGTCTATGGCCCTTGCTTTTATTTAA CCAATAATCTTTTGTATATTTATACCTG 4796
Db 5627 GGAAGTGTCTATGGCCCTTGCTTTTATTTAA CCAATAATCTTTTGTATATTTATACCTG 5686
QY 4797 TTAAAAATTCAGAAATGCAAGCGCGGCACGGTGGCTCACCCCTGTAAATCCACACTT 4856
Db 5687 TTAAAAATTCAGAAATGCAAGCGCGGCACGGTGGCTCACCCCTGTAAATCCACACTT 5746
QY 4857 TGGGAGGCGGAGCGGGTGGTCAACAAGTTCAGGAGTTTGAGACCAAGCCTGACCAACATGG 4916
Db 5747 TGGGAGGCGGAGCGGGTGGTCAACAAGTTCAGGAGTTTGAGACCAAGCCTGACCAACATGG 5806
QY 4917 TGAACCCGCTCTCTAAAAAATACAAAAATTAGCTGGTCA CAGTCAATCGGCACCTGTAGT 4976
Db 5807 TGAACCCGCTCTCTAAAAAATACAAAAATTAGCTGGTCA CAGTCAATCGGCACCTGTAGT 5866
QY 4977 CCCAGCTAAATTGGAGGCTGAGGC 5000
Db 5867 CCCAGCTAAATTGGAGGCTGAGGC 5890

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:14:23 ; Search time 2556.69 Seconds
(without alignments)
11576.980 Million cell updates/sec

Title: US-09-497-957-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 TCTAAGTTGAGATAAAATT.....GCTAATTGAGGCTGAGGC 5000

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5000	100.0	10825	5	AAC68426 Human her
2	5000	100.0	10825	5	AAC68425 Human her
3	5000	100.0	10825	10	ADG87260 Hereditar
4	5000	100.0	10825	10	ADG87262 Hereditar
5	4998.4	100.0	10824	10	ADG87266 Hereditar
6	4998.4	100.0	10825	5	AAC68427 Human her
7	4998.4	100.0	10825	5	AAC68428 Human her
8	4998.4	100.0	10825	10	ADG87264 Hereditar
9	4995.2	99.9	10824	10	ADG87338 Hereditar
10	4995.2	99.9	10825	2	AAT96690 Hereditar
11	4988	99.8	235033	2	AAV57926 Hereditar
12	4957.2	99.1	12146	3	AAV96794 Genomic D
13	4938	98.8	237326	2	AAV57903 Hereditar
14	4607.8	92.2	5982	8	ABV93934 Human col
15	2556.4	51.1	8622	6	ABL34142 Human imm
16	2248.8	45.0	8622	6	ABL34143 Human imm
17	998.4	20.0	5749	8	ABL36747 Human mus
18	998.4	20.0	5749	8	ABX59735 cDNA enco
19	998.4	20.0	5749	12	ADJ30485 Human mus
20	500	10.0	500	12	ACH76934 Human gen

21	420.6	8.4	497	9	ACH27480	Ach27480 Human adu
22	321.2	6.4	32148	4	ABL04218	Abl04218 Human rep
23	321	6.4	1317	6	ABK49917	Abk49917 DNA enco
24	321	6.4	1439	10	ADG87268	Adg87268 Hereditar
25	321	6.4	1439	10	ADG87269	Adg87269 Hereditar
26	321	6.4	1440	2	AAT96691	Aat96691 Hereditar
27	321	6.4	1440	5	AAC68430	Aac68430 Human her
28	321	6.4	1440	5	AAC68429	Aac68429 Human her
29	321	6.4	2506	3	AAV96769	Aav96769 cDNA sequ
30	321	6.4	2727	2	AAV23525	Aav23525 Haemochro
31	321	6.4	2727	11	ADP64956	Adp64956 Human hem
32	321	6.4	2727	11	ADP65373	Adp65373 Human hae
33	319.4	6.4	1439	10	ADG87336	Adg87336 Hereditar
34	319.4	6.4	1439	10	ADG87270	Adg87270 Hereditar
35	319.4	6.4	1439	10	ADG87271	Adg87271 Hereditar
36	319.4	6.4	1440	5	AAC68431	Aac68431 Human her
37	319.4	6.4	1440	5	AAC68432	Aac68432 Human her
38	316.8	6.3	143973	11	ACN44142	Acn44142 Human gen
39	316.6	6.3	2285	13	ADQ38608	Adq38608 Human SNP
40	316.6	6.3	2674	13	ADQ38604	Adq38604 Human SNP
41	316.6	6.3	2716	13	ADQ38602	Adq38602 Human SNP
42	312.4	6.2	46765	6	AAV99306	Aav99306 DNA enco
43	312.4	6.2	126990	12	ADP13332	Adp13332 Renal cel
44	312	6.2	80928	12	ADO25290	Ado25290 Human pro
45	308.8	6.2	78539	8	ACA64942	Aca64942 Human FRA

ALIGNMENTS

RESULT 1
AAC68426
ID AAC68426 standard; DNA; 10825 BP.
XX
AC AAC68426;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-00834497.
XX
PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
(BIRA) BIO-RAD LAB INC.
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
WPI; 2001-006341/01.
XX
P-PSDB; AAB36870.
XX
New hereditary hemochromatosis gene products or polypeptides, useful for
treating hereditary hemochromatosis in a patient, and as a metal
chelation agent alleviating iron overload.
XX
Disclosure; Fig 3; 108pp; English.
XX
The present invention relates to hereditary hemochromatosis gene
products. These proteins may be used to treat a patient diagnosed as
having human hemochromatosis disease. It is also useful as a metal
chelation agent or as a T-cell differentiation factor, and for

CC	alleviating iron overload. They may also be used in protein replacement									
CC	therapy for individuals having a defective human hemochromatosis gene									
XX										
SQ	Sequence	10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 U; 0 Other;								
	Query Match	100.0%; Score 5000; DB 5; Length 10825;								
	Best Local Similarity	100.0%; Pred. No. 0;								
	Matches 5000; Conservative	0; Mismatches 0; Indels 0; Gaps 0;								
QY	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATAAAATATTTA	60							
DB	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATAAAATATTTA	60							
QY	61	AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCGCCAATCAACAACCCCT	120							
DB	61	AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCGCCAATCAACAACCCCT	120							
QY	121	TCAGGATTTAAACCAAGGGGACACTGGATCAGCTAGTGTCTTTCACAAGCAGGTACCTT	180							
DB	121	TCAGGATTTAAACCAAGGGGACACTGGATCAGCTAGTGTCTTTCACAAGCAGGTACCTT	180							
QY	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGTGCTTTTTCACAGGAAGTT	240							
DB	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGTGCTTTTTCACAGGAAGTT	240							
QY	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG	300							
DB	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG	300							
QY	301	TTTTCCCCCCCCAAAAGAGCGAGATTTAAACGGGACGTCGGCCAGAGCTGGGGAA	360							
DB	301	TTTTCCCCCCCCAAAAGAGCGAGATTTAAACGGGACGTCGGCCAGAGCTGGGGAA	360							
QY	361	ATGGGCGCGAGCGAGCGCGCTTCTCCTCTGTATGCTTTTTCAGACCGCGTCTCTG	420							
DB	361	ATGGGCGCGAGCGAGCGCGCTTCTCCTCTGTATGCTTTTTCAGACCGCGTCTCTG	420							
QY	421	CAGGGGCGCTTGCTGCTGAGTCCGAGGCTGCGGGCGAACTAGGGGCGCGGGGGTG	480							
DB	421	CAGGGGCGCTTGCTGCTGAGTCCGAGGCTGCGGGCGAACTAGGGGCGCGGGGGTG	480							
QY	481	GAATAATCGAACTAGCTTTTCTTTCGCGCTTGGGAGTTTGCTAACTTTTGAGGACCTGC	540							
DB	481	GAATAATCGAACTAGCTTTTCTTTCGCGCTTGGGAGTTTGCTAACTTTTGAGGACCTGC	540							
QY	541	TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC	600							
DB	541	TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC	600							
QY	601	CTACCACTGAATCGACATAGGGTCCCTCGCCCCAGGACCTGCCCTCCCGCGGCTGT	660							
DB	601	CTACCACTGAATCGACATAGGGTCCCTCGCCCCAGGACCTGCCCTCCCGCGGCTGT	660							
QY	661	CCGGCTCTCGGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCGCCCACTAGAAATGCTTT	720							
DB	661	CCGGCTCTCGGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCGCCCACTAGAAATGCTTT	720							
QY	721	TAAATAAATCTGTAAGTTCCTCACTTGAGCTGAGCTAAGCTCGGGGCTCTTTGAACCTGG	780							
DB	721	TAAATAAATCTGTAAGTTCCTCACTTGAGCTGAGCTAAGCTCGGGGCTCTTTGAACCTGG	780							
QY	781	AACTCGGGTTTATTTCCAAATGTACAGTGTGAGTTTTTTCGCCAGTCACTCTCCAAACAGG	840							
DB	781	AACTCGGGTTTATTTCCAAATGTACAGTGTGAGTTTTTTCGCCAGTCACTCTCCAAACAGG	840							
QY	841	AAGTTCTTCCCTGAGTGTCTGCCGAGAGGCTGAGCAAAACCAACAGCAGGATCCGCACGG	900							
DB	841	AAGTTCTTCCCTGAGTGTCTGCCGAGAGGCTGAGCAAAACCAACAGCAGGATCCGCACGG	900							
QY	901	GGTTTTCACCTCAGAAAGCAATGCGTTGGCGGTGGGGCGGGAAGAGTGGCGTTGGGGA	960							
DB	901	GGTTTTCACCTCAGAAAGCAATGCGTTGGCGGTGGGGCGGGAAGAGTGGCGTTGGGGA	960							

Qy	961	TCTGAATTCITTCACCATTCACCCACTTTTGGTGAGACCTGGGTGGAGGTCTCTAGGGT	1020
Db	961	TCTGAATTCITTCACCATTCACCCACTTTTGGTGAGACCTGGGTGGAGGTCTCTAGGGT	1020
Qy	1021	GGGAGGCTCCTGAGAGAGGCTTACTCGGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080
Db	1021	GGGAGGCTCCTGAGAGAGGCTTACTCGGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080
Qy	1081	GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACCTGAACTCAAACTCTCTTTTCGG	1140
Db	1081	GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACCTGAACTCAAACTCTCTTTTCGG	1140
Qy	1141	CTAGGCTTTATTTGATTTTGCATGTCTGTAAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Db	1141	CTAGGCTTTATTTGATTTTGCATGTCTGTAAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Qy	1201	TAAATGAACATTAAGCAATGACCTCATTCTTAAAGTTACATTCATATCTGATCTTATTTGA	1260
Db	1201	TAAATGAACATTAAGCAATGACCTCATTCTTAAAGTTACATTCATATCTGATCTTATTTGA	1260
Qy	1261	TTTTCACTAGGATAGGAGGTAGAGCTAATAATACGTTTATTTTACTAGAAGTAACT	1320
Db	1261	TTTTCACTAGGATAGGAGGTAGAGCTAATAATACGTTTATTTTACTAGAAGTAACT	1320
Qy	1321	GGAAATTCAGATTATATAACTCTTTTTCAGGTTTACAAAGAACATAAATAATCTGTTTCTG	1380
Db	1321	GGAAATTCAGATTATATAACTCTTTTTCAGGTTTACAAAGAACATAAATAATCTGTTTCTG	1380
Qy	1381	ATGTTATTTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTGACAGTGATTTTGGCCCTGTAG	1440
Db	1381	ATGTTATTTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTGACAGTGATTTTGGCCCTGTAG	1440
Qy	1441	TGTAGCAGATGTTCTGTGGTTCACGCCCGCTCAGCACAGCACTTTGAGTTTGGTA	1500
Db	1441	TGTAGCAGATGTTCTGTGGTTCACGCCCGCTCAGCACAGCACTTTGAGTTTGGTA	1500
Qy	1501	CTAGTGTATCCACATTTTACACATGACAAGATGAGGCATGGCAGCCCTGCTTCCCTGG	1560
Db	1501	CTAGTGTATCCACATTTTACACATGACAAGATGAGGCATGGCAGCCCTGCTTCCCTGG	1560
Qy	1561	CAAAATTTATTCATTTGCTACACTGGGCTTTGCTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
Db	1561	CAAAATTTATTCATTTGCTACACTGGGCTTTGCTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
Qy	1621	TATGATTTTAAACATACACACTGCAATTAGAGTTGAATAATAAATTTTCTGTTGAGCAG	1680
Db	1621	TATGATTTTAAACATACACACTGCAATTAGAGTTGAATAATAAATTTTCTGTTGAGCAG	1680
Qy	1681	AAATATTCATTTTACAAGTGAATGAGTCCAGGCCATGTTTGCACTGTTCAAGCCC	1740
Db	1681	AAATATTCATTTTACAAGTGAATGAGTCCAGGCCATGTTTGCACTGTTCAAGCCC	1740
Qy	1741	CAAGGAGAGAGCAGGGAAACAAGTCTTTTACCTTTTGATATTTTGCACTTAGTGGGAGA	1800
Db	1741	CAAGGAGAGAGCAGGGAAACAAGTCTTTTACCTTTTGATATTTTGCACTTAGTGGGAGA	1800
Qy	1801	GATGACAAATGAAGAAATGAGCAGAAAGATATACAACTACAGAAATCATGGGTGTTGTA	1860
Db	1801	GATGACAAATGAAGAAATGAGCAGAAAGATATACAACTACAGAAATCATGGGTGTTGTA	1860
Qy	1861	GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTTGAGCAGAGACATGAAGGA	1920
Db	1861	GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTTGAGCAGAGACATGAAGGA	1920
Qy	1921	AATAAGAAATGATATTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTTGGCAAG	1980
Db	1921	AATAAGAAATGATATTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTTGGCAAG	1980
Qy	1981	TTGATTTAAAGCGGGTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGGG	2040
Db	1981	TTGATTTAAAGCGGGTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGGG	2040
Qy	2041	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCTCTGT	2100

Db 2041 CCGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100
Qy CCTCCCTACTCACTAGGTGCTAGGACATCCCCAGTCTTTGACAAACCAAAAATGTCTCT 2160
Db CCTCCCTACTCACTAGGTGCTAGGACATCCCCAGTCTTTGACAAACCAAAAATGTCTCT 2160
Qy AAACCTTTGGCCATGTCACTAGTAGACAACTCCTGGTTAAGAAAGCTGGGTTGAAAA 2220
Db AAACCTTTGGCCATGTCACTAGTAGACAACTCCTGGTTAAGAAAGCTGGGTTGAAAA 2220
Qy AATAAACAAGTGTCTGGGAGTAGAGGCAAGAGTAGGTAAATGGGCTCAGAAAGGA 2280
Db AATAAACAAGTGTCTGGGAGTAGAGGCAAGAGTAGGTAAATGGGCTCAGAAAGGA 2280
Qy GCCAACAACAAGTGTGCAAGGCGCTGTAGGCTGTGTGTGAATTTCTAGCCCAAGAGTA 2340
Db GCCAACAACAAGTGTGCAAGGCGCTGTAGGCTGTGTGTGAATTTCTAGCCCAAGAGTA 2340
Qy ACAGTATCTGTCAAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGACGAATG 2400
Db ACAGTATCTGTCAAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGACGAATG 2400
Qy AAGGAGCAACACTAAAGCAGGAGCCAGCCAGGAAGCTGTTCACAGTCCAGCAAG 2460
Db AAGGAGCAACACTAAAGCAGGAGCCAGCCAGGAAGCTGTTCACAGTCCAGCAAG 2460
Qy AGGTAGTGGAGTGGGCTGGTGGCAACAGAAAAGGAGTGACAAAACATTTGCTCTGAA 2520
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Qy TATATTTCTGAAGAAAGTGTCTGAAGATTCTATGTTGTGTGAGAGAAAGAGAAATGG 2580
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Qy CTGGGTGTAGTACTCATGCCAAGAGGAGGCCAAGAGAGACGATTTCTGTAGCTCAGGA 2640
Db CTGGGTGTAGTACTCATGCCAAGAGGAGGCCAAGAGAGACGATTTCTGTAGCTCAGGA 2640
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Db GTTCAAGACAGGCTGGGCAACACAGCAAAACCCCTTCTACAAAATAACAAAATTA 2700
Qy GCTGGTGTGTGGCATGCACTGTGATCTAGTACTCGGAGGCTGAGGTGGGGTA 2760
Db GCTGGTGTGTGGCATGCACTGTGATCTAGTACTCGGAGGCTGAGGTGGGGTA 2760
Qy TTGCTTGAGCCCAAGGAGTTGAGGCTGCAAGTGAAGCCATGCTGTGCCACTGTACTTCAGC 2820
Db TTGCTTGAGCCCAAGGAGTTGAGGCTGCAAGTGAAGCCATGCTGTGCCACTGTACTTCAGC 2820
Qy CTAGGTGACAGAGAACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGAGTTAAAGT 2880
Db CTAGGTGACAGAGAACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGAGTTAAAGT 2880
Qy TGACTTTGTTCTTTATTTTAAATTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
Db TGACTTTGTTCTTTATTTTAAATTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
Qy TTCTGAGATGGTAAGGCAAGAGAAAGACGATTTGGGGTAATTCAGAGATCTGCATTTG 3000
Db TTCTGAGATGGTAAGGCAAGAGAAAGACGATTTGGGGTAATTCAGAGATCTGCATTTG 3000
Qy GGACATGTTAAGTTTGTAGATTCAGTCCAGGCTTCCAGTGTGAGGCCACATAGGAGTT 3060
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Qy CAGTGTAAAGATTCCAGAACAGGCTGGGCAAGGCTGGCTCACTCTGTAAATCCAGCACT 3120
Db CAGTGTAAAGATTCCAGAACAGGCTGGGCAAGGCTGGCTCACTCTGTAAATCCAGCACT 3120
Qy TTGGTGGCTGAGGCAAGGATGATCAATTTGAGGTGAGGATTTGAGCAAGCTTTGGCCAACA 3180
Db TTGGTGGCTGAGGCAAGGATGATCAATTTGAGGTGAGGATTTGAGCAAGCTTTGGCCAACA 3180

Db 3121 TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3180
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3180
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3240
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3300
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Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3360
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3420
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3420
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3480
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3480
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3540
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3540
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3600
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3600
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3660
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3660
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Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3720
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Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3840
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 3840
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Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 4200
Qy TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 4260
Db TTGGTGGCTGAGGCAAGGATAGATCAATTTGAGGTGAGGATTTGAGACAAGCTTTGGCCAACA 4260

QY 4261 GCCTGTGAATGCAGAGAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
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QY 4321 CAGGACACACCTTGAATTCCTGCCTGCACACACTGGATTGGAGAGCAGCAGAACCCAGGGCC 4380
Db 4321 CAGGACACACCTTGAATTCCTGCCTGCACACACTGGATTGGAGAGCAGCAGAACCCAGGGCC 4380
QY 4381 TGGCCCAACCAAGCTCGAGTGGGAAGGACAAAGATTTCGGGCCAGGCAGAGCCCTTAC 4440
Db 4381 TGGCCCAACCAAGCTCGAGTGGGAAGGACAAAGATTTCGGGCCAGGCAGAGCCCTTAC 4440
QY 4441 CTGGAGAGGAGTGCCTCTGCACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTGTTTG 4500
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Db 4501 GACCAACAAGGTATGTTGGAAACACACTTCTGCCCTTATCTACTAGTGCAGAGTGGAGG 4560
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QY 4681 TGAGACAGCCACAAGTCAATGGGTTTAAATTTCTTCTCATGCATATGGCTCAAGGGAA 4740
Db 4681 TGAGACAGCCACAAGTCAATGGGTTTAAATTTCTTCTCATGCATATGGCTCAAGGGAA 4740
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Db 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTGTATATTTATACCTGTAA 4800
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Db 4801 AAATTCAGAAATGTCAAGCCGGGACGCTGAGTGTGCTCACCCTGTATATCCAGCACTTTGG 4860
QY 4861 AGCCGAGCGGGTGGTCAAGAGTCAAGAGTTCAGAGTTCAGAGCCAGCTGACCAACATGGTGA 4920
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RESULT 2

ID AAC68425 standard; DNA; 10825 BP.

XX AAC68425;

AC AAC68425;

XX 21-FEB-2001 (first entry)

DT 21-FEB-2001 (first entry)

XX Human hereditary hemochromatosis DNA.

XX HH; hereditary hemochromatosis; chelation agent;

KW T-cell differentiation factor; iron overload; ds.

XX Homo sapiens.

XX US6140305-A.

PN 31-OCT-2000.

PD 31-OCT-2000.

XX

PF 04-APR-1997; 97US-00834497.
XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Teuchihashi Z, Wolff RK;
PI Feder JN;
PI WPI; 2001-006341/01.
XX P-PSDB; AAB36869.
DR New hereditary hemochromatosis gene products or polypeptides, useful for
XX treating hereditary hemochromatosis in a patient, and as a metal
XX chelation agent alleviating iron overload.
XX Disclosure; Fig 3; 108pp; English.
XX The present invention relates to hereditary hemochromatosis gene
XX products. These proteins may be used to treat a patient diagnosed as
XX having human hemochromatosis disease. It is also useful as a metal
XX chelation agent or as a T-cell differentiation factor, and for
XX alleviating iron overload. They may also be used in protein replacement
XX therapy for individuals having a defective human hemochromatosis gene
XX
SQ Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 U; 0 Other;
Query Match 100.0%; Score 5000; DB 5; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTAAGTTGAGATAAAATTTTAAATGATATGATGAAATTTTGAATAATTTGAAAAATCATAAATATTTA 60
Db 1 TCTAAGTTGAGATAAAATTTTAAATGATATGATGAAATTTTGAATAATTTGAAAAATCATAAATATTTA 60
QY 61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 120
Db 61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 120
QY 121 TCAGGATTTAAAAACCAAGGGGGACACCTGGATCACCTAGTGTGTTTCAAGCAGAGTACCTT 180
Db 121 TCAGGATTTAAAAACCAAGGGGGACACCTGGATCACCTAGTGTGTTTCAAGCAGAGTACCTT 180
QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACCAGGAAGTT 240
Db 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACCAGGAAGTT 240
QY 241 TTACTGGGCATCTCCTGAGCCTTAGCAATAGCTGTAGGTGACTTCTGAGGCATCCCG 300
Db 241 TTACTGGGCATCTCCTGAGCCTTAGCAATAGCTGTAGGTGACTTCTGAGGCATCCCG 300
QY 301 TTTTCCCGCCCCCAAAAGAGCGAGATTTAAACGGGACGTCGCGCCAGAGCTGGGAA 360
Db 301 TTTTCCCGCCCCCAAAAGAGCGAGATTTAAACGGGACGTCGCGCCAGAGCTGGGAA 360
QY 361 ATGGGCCCGGAGCCAGCCCGGCTTCTCCTCTGATGCTTTTTCAGACCGCGGTCTTG 420
Db 361 ATGGGCCCGGAGCCAGCCCGGCTTCTCCTCTGATGCTTTTTCAGACCGCGGTCTTG 420
QY 421 CAGGGCGCTTGTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 480
Db 421 CAGGGCGCTTGTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 480
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGAGTTTGTAACTTTGGAGGACCTGC 540
Db 481 GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGAGTTTGTAACTTTGGAGGACCTGC 540
QY 541 TCAACCTATCGGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 600
Db 541 TCAACCTATCGGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 600

QY 601 CTACCACTGAAGTGCAGATAGGGGTCCTCGCCCCCAGGACCTGCCCCCTCCCCCGGCTGT 660
 Db 601 CTACCACTGAAGTGCAGATAGGGGTCCTCGCCCCCAGGACCTGCCCCCTCCCCCGGCTGT 660
 QY 661 CCGGCTCTCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAAATGCTTT 720
 Db 661 CCGGCTCTCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAAATGCTTT 720
 QY 721 TAAATAAATCTCGTAGTCTCTCACTTGAAGTGAAGCTGAGCTGAGGCTCTTGAACCTGG 780
 Db 721 TAAATAAATCTCGTAGTCTCTCACTTGAAGTGAAGCTGAGCTGAGGCTCTTGAACCTGG 780
 QY 781 AACTCGGGTTATTTCCAAATGTCAGCTGTGCAAGTTTTTCCCAAGTCATCTCCAAACAGG 840
 Db 781 AACTCGGGTTATTTCCAAATGTCAGCTGTGCAAGTTTTTCCCAAGTCATCTCCAAACAGG 840
 QY 841 AAGTTCTTCCCTGAGTGCTTGGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG 900
 Db 841 AAGTTCTTCCCTGAGTGCTTGGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG 900
 QY 901 GGTTCACACTCAGAAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGGA 960
 Db 901 GGTTCACACTCAGAAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGGA 960
 QY 961 TCTGAATTTCTCAACCAATCCACCACTTTTGGTGAGACCTGGGGTGAGGTCCTAGGGT 1020
 Db 961 TCTGAATTTCTCAACCAATCCACCACTTTTGGTGAGACCTGGGGTGAGGTCCTAGGGT 1020
 QY 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTCCCACTCTTGGCAATTTGTTCTTTT 1080
 Db 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTCCCACTCTTGGCAATTTGTTCTTTT 1080
 QY 1081 GCTGGAATAATTAAGTATATGTTAGTTTGAAGTTTGAAGTGAACAAATTTCTTTTGG 1140
 Db 1081 GCTGGAATAATTAAGTATATGTTAGTTTGAAGTTTGAAGTGAACAAATTTCTTTTGG 1140
 QY 1141 CTAGGCTTTATGATTTGCAATGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
 Db 1141 CTAGGCTTTATGATTTGCAATGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
 QY 1201 TAATGAACATGAAGCAATGCACTCTTAAGTTTACATTTACATCTGATCTTATTTGA 1260
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 QY 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATACGTTTATTTTACTAGAGTTAACT 1320
 Db 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATACGTTTATTTTACTAGAGTTAACT 1320
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 Db 1321 GGAATTCAGATTAATACTCTTTTCAGGTTTACAAAGAACATAAATAATCTGTTTCTG 1380
 QY 1381 ATGTTATTTCAAGTACTACAGTCTCTTAATCTTAGTTGACAGATTTTGGCTGTAG 1440
 Db 1381 ATGTTATTTCAAGTACTACAGTCTCTTAATCTTAGTTGACAGATTTTGGCTGTAG 1440
 QY 1441 TGTAGCACAGTGTCTGTGGGTACACCGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500
 Db 1441 TGTAGCACAGTGTCTGTGGGTACACCGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500
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 Db 1501 CTACGTTATCCACATTTTACATGACAAAGATAGGATGGCAGCGGCTCTCTCTGG 1560
 QY 1561 CAAATTTTCAATGTTACACTGGGCTTTGGTGAGAGCTCATGTCTCCATCTCATAGC 1620
 Db 1561 CAAATTTTCAATGTTACACTGGGCTTTGGTGAGAGCTCATGTCTCCATCTCATAGC 1620
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 Db 1621 TATGATTTCTTAAACATCACATGCAATGAGGTTGAATAATAAATTTTATGTTGAGCAG 1680
 QY 1681 AAATATTTATTTTAAAGTGTAAATGAGTCCAGCCATGTTGTCACCTGTTCAAGCCC 1740

Db 1681 AAATATTTATTTTAAAGTGTAAATGAGTCCAGCCATGTTGTCACCTGTTCAAGCCC 1740
 QY 1741 CAAGGAGAGAGACAGGAAACAAGTCTTTACCTTTTGAATTTTGCATTTCTAGTGGAGA 1800
 Db 1741 CAAGGAGAGAGACAGGAAACAAGTCTTTACCTTTTGAATTTTGCATTTCTAGTGGAGA 1800
 QY 1801 GATGACAAATGAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA 1860
 Db 1801 GATGACAAATGAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA 1860
 QY 1861 GAAGCAGAGAACTCAGGCAAGTCTCTGGGCTGACACTTGGGAGCAGATGAAGGA 1920
 Db 1861 GAAGCAGAGAACTCAGGCAAGTCTCTGGGCTGACACTTGGGAGCAGATGAAGGA 1920
 QY 1921 AATAAGATGATATTTGACCTGGGAGCAGATATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
 Db 1921 AATAAGATGATATTTGACCTGGGAGCAGATATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
 QY 1981 TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
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 Db 2041 CGGCGTGGGGTGGAAAGGGGACTACCATCTGCACTGATAGGATGTCTAGCAGTATCTGT 2100
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 Db 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTATGTGGAAGAGCAATG 2400
 QY 2401 AAGGAGCAACAGTAAAGAGGAGCCAGCCAGCAAGCTGTTACACAGTCCAGGCAAG 2460
 Db 2401 AAGGAGCAACAGTAAAGAGGAGCCAGCCAGCAAGCTGTTACACAGTCCAGGCAAG 2460
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 Db 2461 AGGTAGTGGAGTGGGCTGGGAGCAAGAAAGGAGTGACAAACCATTGTTCTCTGAA 2520
 QY 2521 TATATTTGAAAGAAATTTGCTGAAGATTTCTATGTTGTGAGAAAGAGAAATTTG 2580
 Db 2521 TATATTTGAAAGAAATTTGCTGAAGATTTCTATGTTGTGAGAAAGAGAAATTTG 2580
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 Db 3181 TGGTGAACCCCATGCTCTACTAAAAATACAAAAATTTAGCTGGTGGTGCGGCAAGCT 3240
 Qy 3241 ATAGTCCCAAGCTTTTCAAGGACCTTTAGGTAGGAGATCCCTTGAACCCAGGAGGTGCAGG 3300
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 Db 3301 TTGAGTGAAGCTGAGATTTGCGCACTGCACTCAGCCTGGGTGATAGAGTCTGT 3360
 Qy 3361 CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 3420
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 Qy 3421 TCTAATTTTCCCTGAGCACTACTCTGAGTTCAACTACCTGCTGAGCACTACTTAAC 3480
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 Qy 3601 ACCCAGGACTGTATATGGAAGAAAGACAGGACTGCACTACCTCTCAAAAAATGAGGA 3660
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 Qy 3661 CCAGACACAGCTGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720
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 Qy 3721 CTCCTACTACATGGTTAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
 Db 3721 CTCCTACTACATGGTTAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
 Qy 3781 CCTCTTCAAGGTGCTCAGACAGGACCTTGGTCTTTCTTGTGTTGAAGCTTTGGGCTA 3840
 Db 3781 CCTCTTCAAGGTGCTCAGACAGGACCTTGGTCTTTCTTGTGTTGAAGCTTTGGGCTA 3840
 Qy 3841 CGTGATGACAGCTGTTGCTGTTCTATGATCATGAGAGTCCCGTGGAGCCCGGAAC 3900
 Db 3841 CGTGATGACAGCTGTTGCTGTTCTATGATCATGAGAGTCCCGTGGAGCCCGGAAC 3900

Qy 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTGAA 3960
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QY 4981 GCTAATTGGAAGCTGAGGC 5000
Db |||||||
4981 GCTAATTGGAAGCTGAGGC 5000

RESULT 3

ADG87260
ID ADG87260 standard; DNA; 10825 BP.

XX AC ADG87260;

XX DT 11-MAR-2004 (first entry)

XX DE Hereditary haemochromatosis (HH) wild-type genomic DNA.

XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
KW cirrhosis; diabetes; illness, gene therapy; hepatotropic; gene;
XX chromosome 6; ds.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT CDS 361..7147

FT /tag= b

FT /product= "Hereditary haemochromatosis wild-type protein"

FT exon 361..436

FT /tag= a

FT intron 437..3761

FT /tag= c

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FT mutation /note= "24d2 mutation"

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FT intron /note= "24d7 mutation"

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XX US2003148972-A1.

XX PD 07-AUG-2003.

XX 02-MAY-2002; 2002US-00138888.

XX 04-APR-1996; 96US-00630912.

XX 16-APR-1996; 96US-00632673.

XX 23-MAY-1996; 96US-00652265.

XX 04-APR-1997; 97US-00834497.

XX 04-FEB-2000; 2000US-00497957.

XX (BIRA) BIO-RAD LAB INC.

XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Teuchihashi Z;

PI Wolff RK;

XX WPI; 2003-897595/82.
DR P-PSDB; ADG87261.
XX
PT New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX
PS Claim 1; SEQ ID NO 1; 122pp; English.
XX
CC The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis wild-type
CC genomic DNA located on chromosome 6.
XX
SQ Sequence 10825 BP; 2998 A; 2252 C; 2648 G; 2927 T; 0 U; 0 Other;
Query Match 100.0%; Score 5000; DB 10; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 4
ADG87262
ID ADG87262 standard; DNA; 10825 BP.


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XX 11-MAR-2004 (first entry)
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XX Hereditary haemochromatosis (HH) 24d1 mutant genomic DNA.
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KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
KW ds.
XX
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XX
XX (BIRA ) BIO-RAD LAB INC.
XX
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
XX Wolff RK;
XX
XX WPI; 2003-897595/82.
XX
XX P-PSDB; ADG87263.
XX
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
XX for treating HH leading to diabetes, cirrhosis, sterility or other
XX serious illnesses.
XX
XX Claim 1; SEQ ID NO 3; 122pp; English.
XX
XX The present invention relates to gene and mutations thereto, that are
XX responsible for the disease hereditary haemochromatosis (HH). Sequences
XX of the invention are useful for treating hereditary haemochromatosis
XX which is an inherited disorder or iron metabolism where the body
XX accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
XX and other serious illnesses. The invention is also useful in gene
XX
```

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CC therapy. The present sequence is hereditary haemochromatosis 24d1 mutant
CC genomic DNA.
XX
XX SQ Sequence 10825 BP; 2998 A; 2254 C; 2648 G; 2925 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5000; DB 10; Length 10825;
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 Db |||||
 QY 4201 TGGTTGCAATTAACAGGCTGGGATTTTTCAGAGTCCCAACACCTGCAAGTCACTCTG 4260
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 QY 4261 GGTGTTGAATTCAGAGAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
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 QY 4321 CAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGGGCC 4380
 Db |||||
 QY 4321 CAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGGGCC 4380
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 QY 4381 TGGCCCAACAGCTGAGTGGGAAGGCAAGATTCGGGCCAGGCAAGAGGCGCTTAC 4440
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 QY 4381 TGGCCCAACAGCTGAGTGGGAAGGCAAGATTCGGGCCAGGCAAGAGGCGCTTAC 4440
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 QY 4801 AATTTTCAGAAATGTCAAGCCGGGACCGGTGGCTCACCCCTGTAATCCAGCAGCTTTGGG 4860
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 Db |||||
 RESULT 6
 AAC68427
 ID AAC68427 standard; DNA; 10825 BP.
 XX AC AAC68427;
 XX AC AAC68427;
 DT 21-FEB-2001 (first entry)
 XX Human hereditary hemochromatosis 24d2 mutation DNA.
 XX HH; hereditary hemochromatosis; chelation agent;
 KW T-cell differentiation factor; iron overload; ds.
 XX Homo sapiens.
 XX US6140305-A.
 PD 31-OCT-2000.
 XX 04-APR-1997; 97US-00834497.
 XX 04-APR-1996; 96US-00630912.
 PR 16-APR-1996; 96US-00632673.
 PR 23-MAY-1996; 96US-00652265.
 XX (BIRA) BIO-RAD LAB INC.
 XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Teuchihaashi Z, Wolff RK;
 PI Feder JN;
 XX WPI; 2001-006341/01.
 DR P-PSDB; AAB36871.
 XX New hereditary hemochromatosis gene products or polypeptides, useful for
 PT treating hereditary hemochromatosis in a patient, and as a metal
 PT chelation agent alleviating iron overload.

XX	Disclosure; Fig 3; 108pp; English.	
PS	The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene	
XX	Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 4998.4; DB 5; Length 10825; Best Local Similarity 100.0%; Pred. No. 0; Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATATAATTTA 60	841 AAGTCTTCCCTGAGTGCTTCCGGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG 900
DB	1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATATAATTTA 60	
QY	61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTCCCAATCAACACCCCT 120	901 GGTTCACCTCAGAACGAATCGTTGGCGGTGGGGCGCGAAAGAGTGGCGTTGGGA 960
DB	61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTCCCAATCAACACCCCT 120	901 GGTTCACCTCAGAACGAATCGTTGGCGGTGGGGCGCGAAAGAGTGGCGTTGGGA 960
QY	121 TCAGGATTTAAACCAAGGGGGACATCGGATCACTAGTGTTTCAAGCAGGTACCTT 180	961 TCTGAATTTCTTCAACATTCACCCACTTTTGGTGAGACTCGGGTGGAGGTCTTAGGGT 1020
DB	121 TCAGGATTTAAACCAAGGGGGACATCGGATCACTAGTGTTTCAAGCAGGTACCTT 180	961 TCTGAATTTCTTCAACATTCACCCACTTTTGGTGAGACTCGGGTGGAGGTCTTAGGGT 1020
QY	181 CTGCTGTAGGAGAGAGAACTAAAGTCTGAAAGACCTGTGTCTTTTCAACGAGAGTT 240	1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTCCCACTCTCTGGCAATTTGTTCTTTT 1080
DB	181 CTGCTGTAGGAGAGAGAACTAAAGTCTGAAAGACCTGTGTCTTTTCAACGAGAGTT 240	1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTCCCACTCTCTGGCAATTTGTTCTTTT 1080
QY	241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGATGGGTGACTCTTGAGCATCCCG 300	1081 GCCTGGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAATTTCTCTTTTCGG 1140
DB	241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGATGGGTGACTCTTGAGCATCCCG 300	1081 GCCTGGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAATTTCTCTTTTCGG 1140
QY	301 TTTTCCCGCCCCAAAGAGCGAGATTTAAACGGGACGTGCGGCGAGAGCTCGGGAA 360	1141 CTAGGCTTTATGATTTCGAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
DB	301 TTTTCCCGCCCCAAAGAGCGAGATTTAAACGGGACGTGCGGCGAGAGCTCGGGAA 360	1141 CTAGGCTTTATGATTTCGAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
QY	361 ATGGGCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 420	1201 TAAATGAACATGTAAGCAATGCACCTCTAAAGTTACATTCATATCTGATCTTAATTTGA 1260
DB	361 ATGGGCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 420	1201 TAAATGAACATGTAAGCAATGCACCTCTAAAGTTACATTCATATCTGATCTTAATTTGA 1260
QY	421 CAGGGCGCTTCTGCTGAGTCCAGGCTCGGGCGAACTAGGGGCGCGCGGGGTG 480	1261 TTTTCACTAGGCATAGGAGGTAGAGCTAATAATACGTTTATTTACTAGAAGTTAACT 1320
DB	421 CAGGGCGCTTCTGCTGAGTCCAGGCTCGGGCGAACTAGGGGCGCGCGGGGTG 480	1261 TTTTCACTAGGCATAGGAGGTAGAGCTAATAATACGTTTATTTACTAGAAGTTAACT 1320
QY	481 GAAAAATCGAACTAGCTTTTCTTGGCTTTGGGAGTTTGTAACTTTGGAGGACCTGC 540	1321 GGAATTCAGATTAATAACTCTTTTCAGTTTACAAGAACATAAATAATCTGTTTTCTG 1380
DB	481 GAAAAATCGAACTAGCTTTTCTTGGCTTTGGGAGTTTGTAACTTTGGAGGACCTGC 540	1321 GGAATTCAGATTAATAACTCTTTTCAGTTTACAAGAACATAAATAATCTGTTTTCTG 1380
QY	541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCGTGGAGGTGC 600	1381 ATGTTATTTCAAGTACTACAGCTCTTAATCTTAGTTGACAGTGATTTTGGCCCTGTAG 1440
DB	541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCGTGGAGGTGC 600	1381 ATGTTATTTCAAGTACTACAGCTCTTAATCTTAGTTGACAGTGATTTTGGCCCTGTAG 1440
QY	601 CTACACATGAATCAGATAGGGTCCCTGCGCCAGGACCTGCCCCCTCCCGGCTGT 660	1441 TGTAGCAGAGTGTCTGTGGGTCAACGCCGCTCTCAGCAGCAGCTTTGAGTTTGGTA 1500
DB	601 CTACACATGAATCAGATAGGGTCCCTGCGCCAGGACCTGCCCCCTCCCGGCTGT 660	1441 TGTAGCAGAGTGTCTGTGGGTCAACGCCGCTCTCAGCAGCAGCTTTGAGTTTGGTA 1500
QY	661 CCGGCTCTGCGGAGTGACTTTTGAACCGCCACTTCCCTTCCCCCACTAGAAATGCTTT 720	1501 CTACGTGATCCACATTTTACATGACAAAGATGAGGATGAGGCGCTGCTTCCCTGG 1560
DB	661 CCGGCTCTGCGGAGTGACTTTTGAACCGCCACTTCCCTTCCCCCACTAGAAATGCTTT 720	1501 CTACGTGATCCACATTTTACATGACAAAGATGAGGATGAGGCGCTGCTTCCCTGG 1560
QY	721 TAAATAAATCTCGTAGTTCCTCACTTGAAGCTGAGCTAAGCCTGGGGCTCTTTGAACCTGG 780	1561 CAAATTTATTCAAATGTTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
DB	721 TAAATAAATCTCGTAGTTCCTCACTTGAAGCTGAGCTAAGCCTGGGGCTCTTTGAACCTGG 780	1561 CAAATTTATTCAAATGTTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY	781 AACTCGGGTTATTTTCAATGTCAGTGTGCAAGTTTTCCTCCAGTCACTCCAAACAGG 840	1621 TATGATTTCTTAAACATCACTGCAATAGAGTTGAATTAATAAATTTCTAGTTGAGCAG 1680
DB	781 AACTCGGGTTATTTTCAATGTCAGTGTGCAAGTTTTCCTCCAGTCACTCCAAACAGG 840	1621 TATGATTTCTTAAACATCACTGCAATAGAGTTGAATTAATAAATTTCTAGTTGAGCAG 1680
QY	841 AAGTTCTTCCCTGAGTGCTTCCGGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG 900	1681 AAAATTTCAATTTTACAAAGTAAATGAGTCCAGCCCATGTGTGCACTGTTCAAGCCC 1740
		1681 AAAATTTCAATTTTACAAAGTAAATGAGTCCAGCCCATGTGTGCACTGTTCAAGCCC 1740
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		1801 GATGCAATAAAGCAATGAGCAGAAAGATATACAACTCAGGAATCATGGGTGTTGTGA 1860
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Db |||||

RESULT 7

AAC68428

ID AAC68428 standard; DNA; 10825 BP.

XX AC AAC68428;

XX AC AAC68428;

XX 21-FEB-2001 (first entry)

DT 21-FEB-2001 (first entry)

XX Human hereditary hemochromatosis 24dl/2 mutation DNA.

DE HH; hereditary hemochromatosis; chelation agent;

XX KW T-cell differentiation factor; iron overload; de.

XX KW T-cell differentiation factor; iron overload; de.

XX Homo sapiens.
OS US6140305-A.
XX 31-OCT-2000.
XX 04-APR-1997; 97US-00834497.
XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Teuchihaishi Z, Wolff RK;
PI Feder JN;
XX WPI; 2001-006341/01.
DR P-PSDB; AAB36872.
XX New hereditary hemochromatosis gene products or polypeptides, useful for
PT treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX Disclosure; Fig 3; 108pp; English.
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX
SQ Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 U; 0 Other;
Query Match 100.0%; Score 4998.4; DB 5; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCTAAGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATATATTTA 60
Db |||||
QY 1 TCTAAGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATATATTTA 60
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QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACAGGAAGTT 240
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QY 241 TTACTGGGCATCTCCTGAGCCTTAGCAATAGCTGTAGGGTGAATTTCTGGAGCATCCCCG 300
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Db |||||
QY 421 CAGGGCCGCTTGTGCTGAGTCCGAGGCTCGCGGCGAATAGGGGCGCGCGGGGTG 480
Db |||||
QY 421 CAGGGCCGCTTGTGCTGAGTCCGAGGCTCGCGGCGAATAGGGGCGCGCGGGGTG 480
Db |||||
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGGAGTTTGTCTAACTTTTGAGGACCTGCG 540

Db	481	GAATAATCGAACTAGCTTTTCTTTTGGCGCTTGGAGTTTGTAACTTTTGGAGGACCTGC	540
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Db	541	TCAACCCCTATCCGCAAGCCCTCTCCCTACTTTCTCGCTCCAGACCCCGTGAGGGAGTGC	600
Qy	601	CTACCACTGAACCTGCAGATAGGGGTCCCTCGCCCCCAGGACCTCGCCCCCTCCCGGGCTGT	660
Db	601	CTACCACTGAACCTGCAGATAGGGGTCCCTCGCCCCCAGGACCTCGCCCCCTCCCGGGCTGT	660
Qy	661	CCCGGCTCTCGGAGTGACTTTTGGAAACCCCACTCTCCCTTCCCCCACTAGAAATGCTTT	720
Db	661	CCCGGCTCTCGGAGTGACTTTTGGAAACCCCACTCTCCCTTCCCCCACTAGAAATGCTTT	720
Qy	721	TAAATAAATCTCTAGTCTCTCACTTGAAGCTGAGCTTAAGCTCGGGCTCTTCAACCTGG	780
Db	721	TAAATAAATCTCTAGTCTCTCACTTGAAGCTGAGCTTAAGCTCGGGCTCTTCAACCTGG	780
Qy	781	AACTCGGGTTTATTTCCAAATGTGAGCTGTGAGCTTTTTCCTCCAGTCACTCTCCAAACAGG	840
Db	781	AACTCGGGTTTATTTCCAAATGTGAGCTGTGAGCTTTTTCCTCCAGTCACTCTCCAAACAGG	840
Qy	841	AAGTTCTTCCCTGAGTCTTCCGAGAAAGCTGAGCAAAACCCACAGCAGGATCCGCACGG	900
Db	841	AAGTTCTTCCCTGAGTCTTCCGAGAAAGCTGAGCAAAACCCACAGCAGGATCCGCACGG	900
Qy	901	GGTTTCCACCTCAGAACGAATGGTTGGCGGTGGGGCGCGGAAAGAGTGGGTTGGGA	960
Db	901	GGTTTCCACCTCAGAACGAATGGTTGGCGGTGGGGCGCGGAAAGAGTGGGTTGGGA	960
Qy	961	TCTGAATTTCTTCAACCTTCCACCCACTTTTGTGTGAGACCTTGGGGTGGAGTCTCTAGGGT	1020
Db	961	TCTGAATTTCTTCAACCTTCCACCCACTTTTGTGTGAGACCTTGGGGTGGAGTCTCTAGGGT	1020
Qy	1021	GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTTCCCACTCTTGGGTGAGGCTCTTAGGGT	1080
Db	1021	GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTTCCCACTCTTGGGTGAGGCTCTTAGGGT	1080
Qy	1081	GCTCGAAATTAAGTATATGTAGTTTGAACGTTTGAACGTTTGAACGTTTGAACGTTTGAAC	1140
Db	1081	GCTCGAAATTAAGTATATGTAGTTTGAACGTTTGAACGTTTGAACGTTTGAACGTTTGAAC	1140
Qy	1141	CTAGGCTTTATGATTTGCAATGTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Db	1141	CTAGGCTTTATGATTTGCAATGTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Qy	1201	TAAAGAACATGTAAGCAATGCACTCTTCAAGTTACATTCATATCTGATCTGATTTTGA	1260
Db	1201	TAAAGAACATGTAAGCAATGCACTCTTCAAGTTACATTCATATCTGATCTGATTTTGA	1260
Qy	1261	TTTTCACTAGGCATAGGGAGTAGGAGCTAATAATACGTTTATTTTACTAGAGTTAACT	1320
Db	1261	TTTTCACTAGGCATAGGGAGTAGGAGCTAATAATACGTTTATTTTACTAGAGTTAACT	1320
Qy	1321	GGAAATTCAGATTAATAAATCTTTTTCAGGTTACAAAGAACATAAATAAATCTGTTTCTG	1380
Db	1321	GGAAATTCAGATTAATAAATCTTTTTCAGGTTACAAAGAACATAAATAAATCTGTTTCTG	1380
Qy	1381	ATGTTATTTCAAGTACTACAGTCTTCTAAATCTTTAGTTGACAGTGAATTTGCCCCGTAG	1440
Db	1381	ATGTTATTTCAAGTACTACAGTCTTCTAAATCTTTAGTTGACAGTGAATTTGCCCCGTAG	1440
Qy	1441	TGTAGCACAGTGTCTGTGGGTACACGCGGCTCAGCACAGCCTTTTGAAGTTTGGTA	1500
Db	1441	TGTAGCACAGTGTCTGTGGGTACACGCGGCTCAGCACAGCCTTTTGAAGTTTGGTA	1500
Qy	1501	CTACGTGTATCCACATTTTACACATGACAAAGATGAGGATGCGACGGCTGCTCCTGG	1560
Db	1501	CTACGTGTATCCACATTTTACACATGACAAAGATGAGGATGCGACGGCTGCTCCTGG	1560
Qy	1561	CAAAATTTATCAATGTGACATGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
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Qy	1681	AAATATTTCAATGTTTAAAGTGTAAATGAGTCCCAGCCATGTGTTCACATGTTTCAAGCCC	1740
Db	1681	AAATATTTCAATGTTTAAAGTGTAAATGAGTCCCAGCCATGTGTTCACATGTTTCAAGCCC	1740
Qy	1741	CAAGGAGAGAGCAGGAAACAAAGTCTTTTACCCCTTTGATATTTTGTCAATTTCTAGTGGAGA	1800
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Qy	1801	GATGACAAATGAAGCAATGAGCAGAAAGATATCAACATCAGGAAATCATGGGTGTTGTGA	1860
Db	1801	GATGACAAATGAAGCAATGAGCAGAAAGATATCAACATCAGGAAATCATGGGTGTTGTGA	1860
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Db	1861	GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA	1920
Qy	1921	AATAAGAAATGATTTGAATGAGGAGCAATTTTCCAGGCAAACTGAGTGGGCTGCGCAAG	1980
Db	1921	AATAAGAAATGATTTGAATGAGGAGCAATTTTCCAGGCAAACTGAGTGGGCTGCGCAAG	1980
Qy	1981	TTGGGATTTAAAGACGGGTTTTCTCAGCAGTCTCATGTGTGTGTGTGTGTGTGTGTGTGTGT	2040
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Qy	2041	CGGCGTGGGGTGGGAAGGGGAGTACCATCTGTCATGTAGGATGTCTAGCAGTATCTCTGT	2100
Db	2041	CGGCGTGGGGTGGGAAGGGGAGTACCATCTGTCATGTAGGATGTCTAGCAGTATCTCTGT	2100
Qy	2101	CCTCCCTACTCATAGTGTCTAGGAGCACTCCCGCAGCTTGTGACAAACCAAAATGTCTCT	2160
Db	2101	CCTCCCTACTCATAGTGTCTAGGAGCACTCCCGCAGCTTGTGACAAACCAAAATGTCTCT	2160
Qy	2161	AAACTTTTGCACATGTCACTAGTAGACAAACTCTCTGGTTAAGAGCTCGGGTTGAAAAA	2220
Db	2161	AAACTTTTGCACATGTCACTAGTAGACAAACTCTCTGGTTAAGAGCTCGGGTTGAAAAA	2220
Qy	2221	AATAACAAGTAGTCTCGGGAGTAGAGGCCAAGAGTAGTAAATGGGCTCAGAGAGGA	2280
Db	2221	AATAACAAGTAGTCTCGGGAGTAGAGGCCAAGAGTAGTAAATGGGCTCAGAGAGGA	2280
Qy	2281	GCCACAAACAAGGTTGTGAGGCGCTGTGAGGCTGTGAGTGTGAAATTTCTAGCCAAAGGTA	2340
Db	2281	GCCACAAACAAGGTTGTGAGGCGCTGTGAGGCTGTGAGTGTGAAATTTCTAGCCAAAGGTA	2340
Qy	2341	ACAGTGTCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTCTATGTGGAAGAGCAATG	2400
Db	2341	ACAGTGTCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTCTATGTGGAAGAGCAATG	2400
Qy	2401	AAGGAGCAACAAGTAAAAAGCAGGAGCCAGCAGGAGAGCTTGTACACAGTCCAGGCAAG	2460
Db	2401	AAGGAGCAACAAGTAAAAAGCAGGAGCCAGCAGGAGAGCTTGTACACAGTCCAGGCAAG	2460
Qy	2461	AGGTAGTGGAGTGGGCTGGTGGGAAACAGAAAGGAGTGAACAAACCATTTCTCTGAA	2520
Db	2461	AGGTAGTGGAGTGGGCTGGTGGGAAACAGAAAGGAGTGAACAAACCATTTCTCTGAA	2520
Qy	2521	TATATTTCTGAAGGAATTTGCTGAAGATTTCTATGTTGTGTGAGAAAGAGAAATTCG	2580
Db	2521	TATATTTCTGAAGGAATTTGCTGAAGATTTCTATGTTGTGTGAGAAAGAGAAATTCG	2580
Qy	2581	CTGGGTGTAGTGTCTCATGCCAAGGAGGCGCAAGAGGAGCAGATTTCTTGAGCTCAGGA	2640
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RESULT 8
ADG87264
ID ADG87264 standard; DNA; 10825 BP.
XX AC ADG87264;
XX DT 11-MAR-2004 (first entry)
XX DE Hereditary haemochromatosis (HH) 24d2 mutant genomic DNA.
XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
XX KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
XX OS ds.
XX Unidentified.

Key Location/Qualifiers
CDS 361..7147
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FT exon 7107..7147
FT /*tag= l

US2003148972-A1.
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XX 02-MAY-2002; 2002US-00138888.
XX 04-APR-1996; 96US-00630912.
XX 16-APR-1996; 96US-00632673.
XX 23-MAY-1996; 96US-00652265.
XX 04-APR-1997; 97US-00834497.
XX 04-FEB-2000; 2000US-00497957.
XX (BIRA) BIO-RAD LAB INC.
XX Thomas WJ, Drayna DT, .Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
XX Wolff RK;

DR WPI; 2003-897595/82.
DR P-PSDB; ADG87265.
XX
PT New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX
PS Claim 1; SEQ ID NO 5; 122pp; English.
XX
CC The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis 24d2 mutant
CC genomic DNA.
XX
SQ Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 U; 0 Other;
Query Match 100.0%; Score 4998.4; DB 10; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATAAATATTTA 60
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Db 61 AATATCTAAAGTTTCAGATCAGAAACATTTGCGAAGCTACTTTCCCAATCAACACCCCT 120
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Db 601 CTACCACTGAATGAGATAGGGTCCCTTGGCCCCAGAGCCTGCCCCCTTCCCCGGCTGT 660
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QY ATGTTATTTCAAGTACTACAGCTGCTTAATCTTATCTTGTAGTGAGTGATTTTGGCCGTAG 1440
Db ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTATCTTGTAGTGAGTGATTTTGGCCGTAG 1440
QY TGTAGCACAGTGTCTGTGGGTCAACGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500
Db TGTAGCACAGTGTCTGTGGGTCAACGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500
QY CTACGTGATCCACATTTTACATGACAAGAAATGAGGATGGGATGGGCTGCTTCTGG 1560
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QY 1921 AATAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTGGCAAG 1980
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Qy	3001	GGACATGTTAAAGTTTGAGATTCACAGTTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCGAGTT	3060
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Qy	3061	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTCTCTAATCCGAGCACT	3120
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Qy	3121	TTGGTGGCTGAGCGCAGGTAGATCAATTTGAGTGCAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
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Qy	3181	TGTTGAAAACCCCATGTCTACTTAAATAATACAAAATTAGCCCTGGTGTGGTGGCGCACGCCCT	3240
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Qy	3241	ATAGTCCAGGTTTTTCAGGAGGCTTAGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
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Qy	3301	TTGCAGTGAGCTGAGATTTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
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Qy	3421	TCTAATTTGGCCTGAGCACCAATCTCTGAGTTTCAAATCAATGGCTAGACACACCTTTAAC	3480
Db	3421	TCTAATTTGGCCTGAGCACCAATCTCTGAGTTTCAAATCAATGGCTAGACACACCTTTAAC	3480
Qy	3481	ATTTTCTAGAAATCCACAGCTTTTAGTCGAGTCTGTCTAATCATGAGTATTTGGAATAGGAT	3540
Db	3481	ATTTTCTAGAAATCCACAGCTTTTAGTCGAGTCTGTCTAATCATGAGTATTTGGAATAGGAT	3540
Qy	3541	CTGGGGCAGTGAGGGGTTGGCACCACGTGTGGCAGAGAAAAGCAACAAGGAAAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGTTGGCACCACGTGTGGCAGAGAAAAGCAACAAGGAAAAGAGC	3600
Qy	3601	ACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAAAATGAGGA	3660
Db	3601	ACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAAAATGAGGA	3660
Qy	3661	CCGACACAGCTGATGTTGATGAGTTGATGAGGTGTGTGAGGCTCAACATCTGTCTCCC	3720
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Qy	3721	CTCCTACTACATGGTTAAAGGCTTGTGCTCTGTCTCCAGGTTTCACACTCTCTGCACTA	3780
Db	3721	CTCCTACTACATGGTTAAAGGCTTGTGCTCTGTCTCCAGGTTTCACACTCTCTGCACTA	3780
Qy	3781	CCTCTTCAATGGTGCTTCAGACGAGGACTTGTGCTTTTCTTGTTTGAAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCAATGGTGCTTCAGACGAGGACTTGTGCTTTTCTTGTTTGAAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACACAGCTGTTTCGTGTTTCTATGATCATGAGGTGGCGTGTGAGGCCCGGAAC	3900
Db	3841	CGTGGATGACACAGCTGTTTCGTGTTTCTATGATCATGAGGTGGCGTGTGAGGCCCGGAAC	3900
Qy	3901	TCCAATGGGTTTCCAGTAGAAATTTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
Db	3901	TCCAATGGGTTTCCAGTAGAAATTTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
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Db	3961	AGGGTGGGATCACATGTTTCACTGTTGACTTCTGCACTAATATGGAATAATCAACAACAG	4020

QY	4021	CAAGGGTATGTGGAGAGGGGCCCTCACCTCTCTGAGGTGTCTCAGAGCTTTTCATCTTTTC	4080
DB	4021	CAAGGGTATGTGGAGAGGGGCCCTCACCTCTCTGAGGTGTCTCAGAGCTTTTCATCTTTTC	4080
QY	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTTGTGGGACAGGGAAGGGAAG	4140
DB	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTTGTGGGACAGGGAAGGGAAG	4140
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DB	4261	GGCTGTGAAATTCGAAGAAGACAACAGTACCGAGGGCTACTTGGAAATAGGGACCTATTCCCTT	4320
QY	4321	CAGACACACCTTGAATTTCTGCCCTGACACACTCGATTTGGAGACAGCAGAACCCAGGGCC	4380
DB	4321	CAGACACACCTTGAATTTCTGCCCTGACACACTCGATTTGGAGACAGCAGAACCCAGGGCC	4380
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DB	4381	TGGCCCAACCAAGCTTGGAGTGGGAAAGGSCACAAGATTCGGSCCAGGCAAGACGGGCTAC	4440
QY	4441	CTGGAGAGGACCTGCCCTGACACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGTGTTTTG	4500
DB	4441	CTGGAGAGGACCTGCCCTGACACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGTGTTTTG	4500
QY	4501	GACCAACAAGGTATGGTGGAAAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG	4560
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QY	4621	TCCAAATTCCTGGGAAGGACCTTTCTCAATCCTAGAGTCTCTACCTTATATTCAGAGTGA	4680
DB	4621	TCCAAATTCCTGGGAAGGACCTTTCTCAATCCTAGAGTCTCTACCTTATATTCAGAGTGA	4680
QY	4681	TGACACAGCCACAAGTCATGGGTTTAAATTTCTTTTCTCCATGTCATATGGCTCAAGGGGA	4740
DB	4681	TGACACAGCCACAAGTCATGGGTTTAAATTTCTTTTCTCCATGTCATATGGCTCAAGGGGA	4740
QY	4741	GTGTCTATGGCCCTTGCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
DB	4741	GTGTCTATGGCCCTTGCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
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DB	4801	AAATTCAGAAATGTCAAGGCGGGCAGGTTGGCTCAACCTGTAAATCCACGACCTTTGGG	4860
QY	4861	AGGCCGAGGCGGGTGTCAAGCTCAGGAGTTTGGAGCCAGCTCAGCAACATGTGTGA	4920
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QY	4921	ACCGTCTCTAAAAAATACAAAAATTAGCTGTGTCAAGTCAATGCGCACCTGTAGTCCCA	4980
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DB	4981	GCTAATTTGGAAGGCTGAGGC	5000

RESULT 9
ADG87338
ID ADG87338 standard; DNA; 10824 BP.
XX

AC ADG87338;
XX
DT 11-MAR-2004 (first entry)
XX
DE Hereditary haemochromatosis (HH) 24d7 mutant genomic DNA.
XX
XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;
XX ds.
OS Unidentified.
XX
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FH Key Location/Qualifiers
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FT exon 7107..7147
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PN US2003148972-A1.
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XX 07-AUG-2003.
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XX 02-MAY-2002; 2002US-00138888.
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XX 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
PR 04-APR-1997; 97US-00834497.
PR 04-FEB-2000; 2000US-00497957.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
XX Thomas WJ, Drayna DT, Feder JN, Gnrirke A, Ruddy D, Tsuchihashi Z;
PI Wolff RK;
XX
XX WPI; 2003-897595/82.
DR P-PSDB; ADG87337.
XX
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful
PT for treating HH leading to diabetes, cirrhosis, sterility or other
PT serious illnesses.
XX
XX Disclosure; SEQ ID NO 79; 122pb; English.
PS
XX
XX The present invention relates to gene and mutations thereto, that are
CC responsible for the disease hereditary haemochromatosis (HH). Sequences
CC of the invention are useful for treating hereditary haemochromatosis
CC which is an inherited disorder or iron metabolism where the body
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,
CC and other serious illnesses. The invention is also useful in gene
CC therapy. The present sequence is hereditary haemochromatosis 24d7 mutant

CC genomic DNA.
XX
SQ Sequence 10824 BP; 2996 A; 2253 C; 2646 G; 2929 T; 0 U; 0 Other;
Query Match
Best Local Similarity 99.9%; Score 4995.2; DB 10; Length 10824;
Matches 4997; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGGGAGTGC 600
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Qy 601 CTACACCTGAAGTGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCTCCCGCGCTGT 660
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Db 2461 AGGTAGTGGAGTGGGCTGGGAGCAAGAAAGGAGTGACAAACCAATTTGCTCTGAA 2520
Qy 2521 TATATTTGGAAGAAAGTTGCTGAAGGATTTATGTTGTGTGAGAGAAAGAGAAATGG 2580
Db 2521 TATATTTGGAAGAAAGTTGCTGAAGGATTTATGTTGTGTGAGAGAAAGAGAAATGG 2580
Qy 2581 CTGGGTGTAGTACTCATGCCAAGAGAGAGGCCAAGAGAGAGAGATTTCTGTAGCTCAG 2640
Db 2581 CTGGGTGTAGTACTCATGCCAAGAGAGAGGCCAAGAGAGAGAGATTTCTGTAGCTCAG 2640
Qy 2641 GTTCAAGACACAGCTGGGCAACACAGCAAAACCCCTTCTTCAAAAAATACAAAAATTA 2700
Db 2641 GTTCAAGACACAGCTGGGCAACACAGCAAAACCCCTTCTTCAAAAAATACAAAAATTA 2700
Qy 2701 GCTGGGTGTGGGATGCACCTGTGATCTAGCTACTCGGAGGCTGAGGTGGAGGTA 2760
Db 2701 GCTGGGTGTGGGATGCACCTGTGATCTAGCTACTCGGAGGCTGAGGTGGAGGTA 2760
Qy 2761 TTGCTTGAGCCAGAGAGTTGAGGCTGCAGTGAGCCATGCTGTGCACTGTACTTCCAG 2820
Db 2761 TTGCTTGAGCCAGAGAGTTGAGGCTGCAGTGAGCCATGCTGTGCACTGTACTTCCAG 2820
Qy 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAGAGAGAGTAAAGT 2880
Db 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAGAGAGAGTAAAGT 2880
Qy 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
Db 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
Qy 2941 TTTCTAGATGTGAAGGAG 3000
Db 2941 TTTCTAGATGTGAAGGAG 3000
Qy 3001 GGACATGTTAAGTTTGAATTTCCAGTCTAGGCTTCAAGTGTGGGAGAGAGAGAGAGAG 3060
Db 3001 GGACATGTTAAGTTTGAATTTCCAGTCTAGGCTTCAAGTGTGGGAGAGAGAGAGAGAG 3060
Qy 3061 CAGTGTAAAGATTTAGGAGCAAGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
Db 3061 CAGTGTAAAGATTTAGGAGCAAGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
Qy 3121 TTGGTGGCTGAGGAG 3180
Db 3121 TTGGTGGCTGAGGAG 3180

Qy	3181	TGTTGAAACCCCATGTTCTACTAAATAACAATAATTAGCTGTGTGGTGGCCACGCGCT	3240
Db	3181	TGTTGAAACCCCATGTTCTACTAAATAACAATAATTAGCTGTGTGGTGGCCACGCGCT	3240
Qy	3241	ATAGTCCACAGGTTTTACAGGAGCTTAGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
Db	3241	ATAGTCCACAGGTTTTACAGGAGCTTAGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
Qy	3301	TTGCAGTGAAGTGAATTTGTGCCACTGCACCTCAGAGCTGGGTGATAGAGTGAAGACTCTGT	3360
Db	3301	TTGCAGTGAAGTGAATTTGTGCCACTGCACCTCAGAGCTGGGTGATAGAGTGAAGACTCTGT	3360
Qy	3361	CTCAAA	3420
Db	3361	CTCAAA	3420
Qy	3421	TCTAAATTTGGCTGAGACCAACTCTCTGAGTTCACTACCATGGCTAGACACACTTTAAC	3480
Db	3421	TCTAAATTTGGCTGAGACCAACTCTCTGAGTTCACTACCATGGCTAGACACACTTTAAC	3480
Qy	3481	ATTTTCTAGAAATCCACACAGCTTTAGTGGAGTCTGTCTAAATCATGAGTATTGGAATAGGAT	3540
Db	3481	ATTTTCTAGAAATCCACACAGCTTTAGTGGAGTCTGTCTAAATCATGAGTATTGGAATAGGAT	3540
Qy	3541	CTGGGGCAGTGAGGGGGTGGCACCACGTTGTGGCAGAGAAAGACACACAAGGAAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGGTGGCACCACGTTGTGGCAGAGAAAGACACACAAGGAAAGAGC	3600
Qy	3601	ACCAGAGCTGTCTATATGGAAGAAAGACAGGACTGCACTCACCTTCAAAAATGAGGA	3660
Db	3601	ACCAGAGCTGTCTATATGGAAGAAAGACAGGACTGCACTCACCTTCAAAAATGAGGA	3660
Qy	3661	CCAGACACAGCTGATGCTATGAGTTGATGAGTGTGAGGAGCTGAGAGCTCAACATCTGCTCCC	3720
Db	3661	CCAGACACAGCTGATGCTATGAGTTGATGAGTGTGAGGAGCTGAGAGCTCAACATCTGCTCCC	3720
Qy	3721	CTCCTACTACACATGGTTAAGGGCTGTGCTCTGTCTCTCCAGAGTTCAACCTCTCTGCACCTA	3780
Db	3721	CTCCTACTACACATGGTTAAGGGCTGTGCTCTGTCTCTCCAGAGTTCAACCTCTCTGCACCTA	3780
Qy	3781	CCTCTTCAATGGGTGCCCTCAGACAGGAGCTTGGTCTTCTCTGTTTGAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCAATGGGTGCCCTCAGACAGGAGCTTGGTCTTCTCTGTTTGAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACAGCTGTTCGTGTTCTATGATCATGAGAGTGCAGAGTGTGAGAGCCCGAAC	3900
Db	3841	CGTGGATGACAGCTGTTCGTGTTCTATGATCATGAGTGTGAGAGTGTGAGAGCCCGAAC	3900
Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGAGTCTGAA	3960
Db	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGAGTCTGAA	3960
Qy	3961	AGGTTGGGATCACATGTTTCACTGTTGACTTTCTGGACTATTATGAAAAATCACAAACACAG	4020
Db	3961	AGGTTGGGATCACATGTTTCACTGTTGACTTTCTGGACTATTATGAAAAATCACAAACACAG	4020
Qy	4021	CAAGGTTATGTGGAGAGGGGGCTCACCTTCTGTAGGTTGTGAGAGCTTTTCACTCTTTC	4080
Db	4021	CAAGGTTATGTGGAGAGGGGGCTCACCTTCTGTAGGTTGTGAGAGCTTTTCACTCTTTC	4080
Qy	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGGGAAG	4140
Db	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGGAAGGGAAG	4140
Qy	4141	GAATTTGCTTCTCTGAGATCATTTTGGTCCCTTTGGGAGTGGTGAATATGGGACCTATTCCCTT	4200
Db	4141	GAATTTGCTTCTCTGAGATCATTTTGGTCCCTTTGGGAGTGGTGAATATGGGACCTATTCCCTT	4200
Qy	4201	TGTTTGCAGTTAAACAGGCTGGGATTTTTTCCAGAGTCCACACCTTGCAGGTCATCCTG	4260
Db	4201	TGTTTGCAGTTAAACAGGCTGGGATTTTTTCCAGAGTCCACACACCTTGCAGGTCATCCTG	4260

Qy	4261	GGCTGTGAAATGCAAGAGCAACACAGTACCGAGGGCTACTGGAAATGATACGGGTATGATGGG	43220
Db	4261	GGCTGTGAAATGCAAGAGCAACACAGTACCGAGGGCTACTGGAAATGATACGGGTATGATGGG	43220
Qy	4321	CAGGACCAACCTTGAAATTCCTGCCTCTGACACACACTGGATTGGAGAGCAGCAGAACCCAGGGCC	4380
Db	4321	CAGGACCAACCTTGAAATTCCTGCCTCTGACACACACTGGATTGGAGAGCAGCAGAACCCAGGGCC	4380
Qy	4381	TGGCCCCAACAGCTGGAGTGGGAAAGGCCACAAGATTTCGGGCCACAGGCAGAACACGGGCTTAC	4440
Db	4381	TGGCCCCAACAGCTGGAGTGGGAAAGGCCACAAGATTTCGGGCCACAGGCAGAACACGGGCTTAC	4440
Qy	4441	CTGGAGAGGAGCTGCCCTCTGACAGCTGACAGCAGTGTCTCGAGCTGGGGAGAGGTGTTTG	4500
Db	4441	CTGGAGAGGAGCTGCCCTCTGACAGCTGACAGCAGTGTCTCGAGCTGGGGAGAGGTGTTTG	4500
Qy	4501	GACCAACAGGTATGCTGGAAACACACACTTCTGCCCTATACCTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAGGTATGCTGGAAACACACACTTCTGCCCTATACCTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGGTTCAGGGCACCGAATCCCTGGTGTGGAGTTTCAGAGGTGGCTCAGGCTGTGTGCCTC	4620
Db	4561	AGGTTCAGGGCACCGAATCCCTGGTGTGGAGTTTCAGAGGTGGCTCAGAGCTGTGTGCCTC	4620
Qy	4621	TCCAAAATTCGGGAAGGACTTTCTCAATCCTAGAGTCTCTACCTTATTAATTGAGATGTA	4680
Db	4621	TCCAAAATTCGGGAAGGACTTTCTCAATCCTAGAGTCTCTACCTTATTAATTGAGATGTA	4680
Qy	4681	TGAGACAGCCACAGTTCATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAGGGAA	4740
Db	4681	TGAGACAGCCACAGTTCATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAGGGAA	4740
Qy	4741	GTGCTATGCCCCTTGCTTTTATTTTAAACAAATAATCTTTTGATATTTATACCTGTAA	4800
Db	4741	GTGCTATGCCCCTTGCTTTTATTTTAAACAAATAATCTTTTGATATTTATACCTGTAA	4800
Qy	4801	AAATTTCAGAAATGTCAGGCCCGGCACGGTGGCTCACCCCTGTAAATCCAGCACTTTGGG	4860
Db	4801	AAATTTCAGAAATGTCAGGCCCGGCACGGTGGCTCACCCCTGTAAATCCAGCACTTTGGG	4860
Qy	4861	AGCCGAGGGGGTGTGTACAGGTCAGAGTTTGAGACCGGCTGACCAACATGGTGAA	4920
Db	4861	AGCCGAGGGGGTGTGTGTACAGGTCAGAGTTTGAGACCGGCTGACCAACATGGTGAA	4920
Qy	4921	ACCCGCTCTTAAAAAATACAAAATTTAGCTGTGTACAGTCTAGTGGCAGCTGTAGTCCCA	4980
Db	4921	ACCCGCTCTTAAAAAATACAAAATTTAGCTGTGTGTACAGTCTAGTGGCAGCTGTAGTCCCA	4980
Qy	4981	GCTAATTGGAAGGCTGAGGC	5000
Db	4981	GCTAATTGGAAGGCTGAGGC	5000
RESULT 10			
AAT96690			
ID	AAT96690 standard; DNA; 10825 BP.		
XX	AC AAT96690;		
XX	14-APR-1998 (first entry)		
XX	Hereditary haemochromatosis gene.		
DE	Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy;		
KW	prenatal screening; human; ds.		
XX	Homo sapiens.		
OS	Key		
XX	Location/Qualifiers		
FT	361..7147		
FT	/*tag= a		
FT	/note= "contains introns"		
FT	437..3761		

3061 QY CAGGTGAAGAAATTCAGGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT 3120
3061 DB CAGGTGAAGAAATTCAGGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT 3120
3121 QY TTGGTGGCTGAGGCAGGTAGATCATTTTGGAGTTCAGGATTTGAGACAAGCTTTGGCCAAACA 3180
3121 DB TTGGTGGCTGAGGCAGGTAGATCATTTTGGAGTTCAGGATTTGAGACAAGCTTTGGCCAAACA 3180
3181 QY TTGGTGAAGACCCCATGCTCTACTAAAAATACAAAAATTTAGCTGGTGGTGGCGACGCTCT 3240
3181 DB TTGGTGAAGACCCCATGCTCTACTAAAAATACAAAAATTTAGCTGGTGGTGGCGACGCTCT 3240
3241 QY ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGGTGCAGG 3300
3241 DB ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGGTGCAGG 3300
3301 QY TTGCAGTGAGCTGAGATTTGTGCCACTGCACCTCCAGCTGGGTGATAGAGTGAGACTCTGT 3360
3301 DB TTGCAGTGAGCTGAGATTTGTGCCACTGCACCTCCAGCTGGGTGATAGAGTGAGACTCTGT 3360
3361 QY CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3420
3361 DB CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3420
3421 QY TCTAATTTGCCCTGAGCAACAATCTCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC 3480
3421 DB TCTAATTTGCCCTGAGCAACAATCTCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC 3480
3481 QY ATTTTCTAGAAATCCACCACTTTAGTGGAGTCTGTCTAATCATGAGTATTTGAATAGGAT 3540
3481 DB ATTTTCTAGAAATCCACCACTTTAGTGGAGTCTGTCTAATCATGAGTATTTGAATAGGAT 3540
3541 QY CTGGGGGAGTGGAGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAGGAAAGAGC 3600
3541 DB CTGGGGGAGTGGAGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAGGAAAGAGC 3600
3601 QY ACCCAGGACTGTATATGGAAGAAAGACAGGAGCTGCAACTCACCCTTCAAAAAATGAGGA 3660
3601 DB ACCCAGGACTGTATATGGAAGAAAGACAGGAGCTGCAACTCACCCTTCAAAAAATGAGGA 3660
3661 QY CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGGAGGCTCAACATCTGCTGCC 3720
3661 DB CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGGAGGCTCAACATCTGCTGCC 3720
3721 QY CTCCTACTACATGTTTAAAGCCTTGTCTCTGCTCCAGGTTCACACTCTCTGCACTA 3780
3721 DB CTCCTACTACATGTTTAAAGCCTTGTCTCTGCTCCAGGTTCACACTCTCTGCACTA 3780
3781 QY CCTCTTCATGGGTGCTCAGACAGGACCTTGGTCTTTCTTTTGAAGCTTTGGGCTA 3840
3781 DB CCTCTTCATGGGTGCTCAGACAGGACCTTGGTCTTTCTTTTGAAGCTTTGGGCTA 3840
3841 QY CGTGGATGACAGCTGTTGCTGTTCTATGATCATGAGAGTCGCGTGTGGAGCCCGGAAC 3900
3841 DB CGTGGATGACAGCTGTTGCTGTTCTATGATCATGAGAGTCGCGTGTGGAGCCCGGAAC 3900
3901 QY TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 3960
3901 DB TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA 3960
3961 QY AGGGTGGGATCATGTTTCACTGTTGACTTCTGGACTATTATGGAATAATCAACACACAG 4020
3961 DB AGGGTGGGATCATGTTTCACTGTTGACTTCTGGACTATTATGGAATAATCAACACACAG 4020
4021 QY CAAGGGTATGTGGAGAGGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTTTTC 4080
4021 DB CAAGGGTATGTGGAGAGGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTTTTC 4080
4081 QY ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGGCTGCTGGGAGCAGGGAAGGGAAG 4140
4081 DB ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGGCTGCTGGGAGCAGGGAAGGGAAG 4140
4141 QY GAAATTTGCTTCTGAGATCATTTTGGTCTTGGGGATGTTGGAAATAGGACCTATTTCCTT 4200

4141 DB GAAATTTGCTTCTGAGATCATTTTGGTCTTGGGGATGTTGGAAATAGGACCTATTTCCTT 4200
4201 QY TGGTTGCAGTTAAACAAGGCTGGGATTTTCCAGAGTCCCAACCCCTGCAGTCACTCTG 4260
4201 DB TGGTTGCAGTTAAACAAGGCTGGGATTTTCCAGAGTCCCAACCCCTGCAGTCACTCTG 4260
4261 QY GGCTGTGAAATCAAGAAGACAAAGTACCGAGGGCTACTCGGAAGTACGGGTATGATGG 4320
4261 DB GGCTGTGAAATCAAGAAGACAAAGTACCGAGGGCTACTCGGAAGTACGGGTATGATGG 4320
4321 QY CAGGACCACTTTGAATTTCTGCCCTGACACACTTGGATTTGGAGAGCAGACAAACCCAGGCC 4380
4321 DB CAGGACCACTTTGAATTTCTGCCCTGACACACTTGGATTTGGAGAGCAGACAAACCCAGGCC 4380
4381 QY TGGCCCAACCAAGCTGGAGTGGGAAAGGCAAAAGTTCGGGCCAGGCAAGACAGGGCTTAC 4440
4381 DB TGGCCCAACCAAGCTGGAGTGGGAAAGGCAAAAGTTCGGGCCAGGCAAGACAGGGCTTAC 4440
4441 QY CTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTGTCTGGAGTGGGGAGAGGTGTTTGG 4500
4441 DB CTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTGTCTGGAGTGGGGAGAGGTGTTTGG 4500
4501 QY GACCAACAAGGTATGGTGGAAACAACACTTCTGCCCTATATCTCTAGTGGCAGAGTGGAG 4560
4501 DB GACCAACAAGGTATGGTGGAAACAACACTTCTGCCCTATATCTCTAGTGGCAGAGTGGAG 4560
4561 QY AGGTTGCAGGGCAGCGAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTGCCCTC 4620
4561 DB AGGTTGCAGGGCAGCGAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTGCCCTC 4620
4621 QY TCCAAATTTCTGGGAAGGACTTTCTCAATCTCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680
4621 DB TCCAAATTTCTGGGAAGGACTTTCTCAATCTCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680
4681 QY TGAGACAGCCCAAGCTCATGGTTTAAATTTCTTCTCATGCATATGGCTCAAGGGAA 4740
4681 DB TGAGACAGCCCAAGCTCATGGTTTAAATTTCTTCTCATGCATATGGCTCAAGGGAA 4740
4741 QY GTGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTGTTAA 4800
4741 DB GTGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTGTTAA 4800
4801 QY AAATTCAGAAATGTCAAGCCCGGCA CGGTGGCTCACCCCTGTAATCCAGCACTTTGGG 4860
4801 DB AAATTCAGAAATGTCAAGCCCGGCA CGGTGGCTCACCCCTGTAATCCAGCACTTTGGG 4860
4861 QY AGGCCGAGCGGGTGGTCAAGGTTCAGAGTTCAGAGTTCAGACCGCTGACCAACATGGTGA 4920
4861 DB AGGCCGAGCGGGTGGTCAAGGTTCAGAGTTCAGAGTTCAGACCGCTGACCAACATGGTGA 4920
4921 QY ACCCGTCTCTAAAAAATAACAAAATTTAGCTGGTCAAGTCACTGGCAGCTGTAGTCCCA 4980
4921 DB ACCCGTCTCTCTAAAAAATAACAAAATTTAGCTGGTCAAGTCACTGGCAGCTGTAGTCCCA 4980
4981 QY GCTAATTTGGAAGGCTGAGGC 5000
4981 DB GCTAATTTGGAAGGCTGAGGC 5000

RESULT 11

AAV57926/c

ID AAV57926 standard; DNA; 235033 BP.

XX AAV57926;

AC AAV57926;

XX 23-DEC-1998 (first entry)

XX Hereditary haemochromatosis subregion from an unaffected individual.

DE Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;

XX diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4;

KW BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;

KW

KW type 1 sodium transport gene; ss.
XX Homo sapiens.
OS WO9814466-A1.
PN XX
PD XX
PF 30-SEP-1997; 97WO-US017658.
XX 01-OCT-1996; 96US-00724394.
PR 07-MAY-1997; 97US-00852495.
XX (PROG-) PROGENITOR INC.
XX Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
PI Tsuchihashi Z, Wolff RK;
PI WPI; 1998-240014/21.
DR XX
XX Hereditary haemochromatosis gene products - used to develop products for
PT the diagnosis and treatment of hereditary disorders in iron metabolism.
XX
XX Example 2; Fig 8; 209pp; English.
XX
CC The present invention describes hereditary haemochromatosis gene products
CC from the human haemochromatosis gene. The present sequence represents a
CC hereditary haemochromatosis subregion from an individual unaffected by
CC hereditary haemochromatosis (HH). Also described is a method to determine
CC the presence or absence of the common hereditary haemochromatosis (HFE)
CC gene mutation in an individual comprising: (a) providing DNA or RNA from
CC the individual; and (b) assessing the DNA or RNA for the presence or
CC absence of a haplotype or genotype where the presence or absence of the
CC haplotype genotype indicates the likely presence of the HFE gene mutation
CC in the genome of the individual. The HFE gene sequences from the present
CC invention can be used to develop products for use in the diagnosis and
CC treatment of HFE. The present invention also describes BTF genes, which
CC are homologues of the milk protein butyrophilin (BT), and can be used in
CC the production of agonists and antagonists of BTF function. Also described
CC are: (1) a RoRet gene which can be used to develop products for the
CC study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2)
CC NPT3 and NPT4 genes which are homologues of a type 1 sodium transport
CC gene, and can similarly be used for hypophosphatemia
XX
SQ Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 U; 0 Other;

Query Match 99.8%; Score 4988; DB 2; Length 235033;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4999; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATATAATATTTA 60
DB 47148 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATATAATTTA 47089

QY 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAAACCCCT 120
DB 47088 AATACTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAAACCCCT 47029

QY 121 TCAGAGTTTAAAAACAAGGGGGACACTGGATCACCTAGTGTGTTTCAAGCAGGTACCTT 180
DB 47028 TCAGAGTTTAAAAACAAGGGGGACACTGGATCACCTAGTGTGTTTCAAGCAGGTACCTT 46969

QY 181 CTGCTGTAGGAGAGAGAGACTAAAGTTCTGAAGACCTGTGCTTTTCCACGAGAAGTTT 240
DB 46968 CTGCTGTAGGAGAGAGAGACTAAAGTTCTGAAGACCTGTGCTTTTCCACGAGAAGTTT 46909

QY 241 TTACTGGGCATCTCTCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG 300
DB 46908 TTACTGGGCATCTCTCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG 46849

QY 301 TTTCCCGCCCCCAAAAGACGGAGATTTTAAACGGGACGTGCGGCGCAGAGCTGGGAA 360
DB 46848 TTTCCCGCCCCCAAAAGACGGAGATTTTAAACGGGACGTGCGGCGCAGAGCTGGGAA 46789

QY 361 ATGGCCCGCGAGCCAGCCGCGCGCTTCTCTCTGATGCTTTTGACAGCCGCGTCTCG 420
DB 46788 ATGGCCCGCGAGCCAGCCGCGCGCTTCTCTCTGATGCTTTTGACAGCCGCGTCTCG 46729

QY 421 CAGGGCGCTTTGCTGCGTGAAGTCCGAGGGCTGCGGCGAACTAGGGGCGCGCGGGGTG 480
DB 46728 CAGGGCGCTTTGCTGCGTGAAGTCCGAGGGCTGCGGCGAACTAGGGGCGCGCGGGGTG 46669

QY 481 GAAAAATCGAAACTAGCTTTTCTTTGCGTGTGGAGTTTGTCTAATTTTGAGGACCTGTC 540
DB 46668 GAAAAATCGAAACTAGCTTTTCTTTGCGTGTGGAGTTTGTCTAATTTTGAGGACCTGTC 46609

QY 541 TCAACCTTATCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAAGGAGTGC 600
DB 46608 TCAACCTTATCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAAGGAGTGC 46549

QY 601 CTACCACCTGAAGTGCAGATAGGGGTCCCTCGCCCGCAGGACCTGCCCCCTCCCGGCTGT 660
DB 46548 CTACCACCTGAAGTGCAGATAGGGGTCCCTCGCCCGCAGGACCTGCCCCCTCCCGGCTGT 46489

QY 661 CCCGCTCTCGGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGAAATGCTTT 720
DB 46488 CCCGCTCTCGGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGAAATGCTTT 46429

QY 721 TAAATAATCTCGTAGTTCCCTCACTTGAGCTGAGCTAAGCCTGGGCTCCTTGACCTGG 780
DB 46428 TAAATAATCTCGTAGTTCCCTCACTTGAGCTGAGCTAAGCCTGGGCTCCTTGAACTGG 46369

QY 781 AACTCGGGTGTATTTTCCAAATGTGAGCTGTGAGTTTTTTTCCCGAGTCACTCCCAACAGG 840
DB 46368 AACTCGGGTGTATTTTCCAAATGTGAGCTGTGAGTTTTTTTCCCGAGTCACTCCCAACAGG 46309

QY 841 AAGTTTCTCCCTGAGTGTCTCGGAGAAAGCTGAGCAAAACCCACAGCAGGATCCGACGG 900
DB 46308 AAGTTTCTCCCTGAGTGTCTCGGAGAAAGCTGAGCAAAACCCACAGCAGGATCCGACGG 46249

QY 901 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGCGGAAGAGTGGGTTGGGA 960
DB 46248 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGCGGAAGAGTGGGTTGGGA 46189

QY 961 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACTCTGGGGTGGAGTCTCTAGGT 1020
DB 46188 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACTCTGGGGTGGAGTCTCTAGGT 46129

QY 1021 GGGAGGCTCTGAGAGAGGCTTACTCGGGCTTTTCCCACTCTTTGGCAAATGTTCTTTT 1080
DB 46128 GGGAGGCTCTGAGAGAGGCTTACTCGGGCTTTTCCCACTCTTTGGCAAATGTTCTTTT 46069

QY 1081 GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACCTGAACAATTTCTTTTTCGG 1140
DB 46068 GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACCTGAACAATTTCTTTTTCGG 46009

QY 1141 CTAGGCTTTATGATTTGCAATGTCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200
DB 46008 CTAGGCTTTATGATTTGCAATGTCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 45949

QY 1201 TAATGAACATGTAGCAATGCACTCACTTCTAAGTTTACATTCATTCATCTGATCTTATTTGA 1260
DB 45948 TAATGAACATGTAGCAATGCACTCACTTCTAAGTTTACATTCATTCATCTGATCTTATTTGA 45889

QY 1261 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAACGTTTATTTTACTAGAAAGTTAACT 1320
DB 45888 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAACGTTTATTTTACTAGAAAGTTAACT 45829

QY 1321 GGAATTCAGATTATATACTCTTTTTCAGGTTTACAAAGAACATAAATAATCTGGTTTCTG 1380
DB 45828 GGAATTCAGATTATATACTCTTTTTCAGGTTTACAAAGAACATAAATAATCTGGTTTCTG 45769

QY 1381 ATGTTATTTCAAGTACTACAGCTGTTCTAATCTTAGTTTGAAGTATTTTGGCCCTGTAG 1440
DB 45768 ATGTTATTTCAAGTACTACAGCTGTTCTAATCTTAGTTTGAAGTATTTTGGCCCTGTAG 45709

QY	1441	TGTAGCACAGTGTCTGTGGGTACACGCGGGCTCAGCACAGCACTTTTGGTGA	1500
Db	45708	TGTAGCACAGTGTCTGTGGGTACACGCGGGCTCAGCACAGCACTTTTGGTGA	45649
QY	1501	CTACGTGTATCCACATTTTACACATGACAGATGAGGCATGCGCTGCTTCTGG	1560
Db	45648	CTACGTGTATCCACATTTTACACATGACAGATGAGGCATGCGCTGCTTCTGG	45589
QY	1561	CAAAATTTATTTCAATGTGACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
Db	45588	CAAAATTTATTTCAATGTGACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	45529
QY	1621	TATGATTTCTTAAACATCACATGCACTAGAGGTGGAATATAAATTTTCACTGTGAGCAG	1680
Db	45528	TATGATTTCTTAAACATCACATGCACTAGAGGTGGAATATAAATTTTCACTGTGAGCAG	45469
QY	1681	AAATATTCAATGTTTACAAAGTGTAAATGATGCCAGCCATGTTGCACTGTTCAAGCCC	1740
Db	45468	AAATATTCAATGTTTACAAAGTGTAAATGATGCCAGCCATGTTGCACTGTTCAAGCCC	45409
QY	1741	CAAGGAGAGAGCAGGGAAACAAGTCTTTTACCTTTTGATATTTTGCATTTCTAGTGGGAGA	1800
Db	45408	CAAGGAGAGAGCAGGGAAACAAGTCTTTTACCTTTTGATATTTTGCATTTCTAGTGGGAGA	45349
QY	1801	GATGACAAATAGCAATGAGCAAGAAAGATATACAAATCAGGAAATCATGGGTGTTGTGA	1860
Db	45348	GATGACAAATAGCAATGAGCAAGAAAGATATACAAATCAGGAAATCATGGGTGTTGTGA	45289
QY	1861	GAGCAGAGAGTCAGGCGAAGTCACTCTGGGGCTGACACTTGGAGCAGACATGAGGA	1920
Db	45288	GAGCAGAGAGTCAGGCGAAGTCACTCTGGGGCTGACACTTGGAGCAGACATGAGGA	45229
QY	1921	AATAAGAAATGATATTCACCTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	1980
Db	45228	AATAAGAAATGATATTCACCTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	45169
QY	1981	TTGGATTTAAAAACGCGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	2040
Db	45168	TTGGATTTAAAAACGCGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	45109
QY	2041	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTACAGTATCCTGT	2100
Db	45108	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTACAGTATCCTGT	45049
QY	2101	CTCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTGACAAACAAAAATGCTCT	2160
Db	45048	CTCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTGACAAACAAAAATGCTCT	44989
QY	2161	AAACTTTGCCACATGTCACTAGTAGACAAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAA	2220
Db	44988	AAACTTTGCCACATGTCACTAGTAGACAAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAA	44929
QY	2221	AATAAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAGAGGA	2280
Db	44928	AATAAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAGAGGA	44869
QY	2281	GCACAAAAAAGTGTCTGAGGCGCTGTAGGCTGTGTGTGAAATTTCTAGCCAAAGAGTA	2340
Db	44868	GCACAAAAAAGTGTCTGAGGCGCTGTAGGCTGTGTGTGAAATTTCTAGCCAAAGAGTA	44809
QY	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAAGCAGAAATG	2400
Db	44808	ACAGTGATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAAGCAGAAATG	44749
QY	2401	AAGGAGACACAGTAAAGCAGGGACCCAGCCAGGAAGCTGTATACAGTCTAGGCAAG	2460
Db	44748	AAGGAGACACAGTAAAGCAGGGACCCAGCCAGGAAGCTGTATACAGTCTAGGCAAG	44689
QY	2461	AGGTAGTGGAGTGGGCTGGGTGGAAACAGAAAGGAGGTGACAAACATTTGCTCTGAA	2520
Db	44688	AGGTAGTGGAGTGGGCTGGGTGGAAACAGAAAGGAGGTGACAAACATTTGCTCTGAA	44629
QY	2521	TATATTTCTGAAGGAAGTGTCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG	2580

Db	44628	TATATTTCTGAAGGAAGTGTCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG	44569
QY	2581	CTGGGTGTAGTAGTCTCATGCCAAGGAGGAGGCCAAGGAGCAGAGTTCCTTGAGCTCAGGA	2640
Db	44568	CTGGGTGTAGTAGTCTCATGCCAAGGAGGAGGCCAAGGAGCAGAGTTCCTTGAGCTCAGGA	44509
QY	2641	GTTTCAAGACACAGCCTCGGGCAACACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
Db	44508	GTTTCAAGACACAGCCTCGGGCAACACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	44449
QY	2701	GCTGGGTGTGGCATGCACTGTGATCTCTAGTCTACTCGGAGAGGCTGAGGTGAGGGTGA	2760
Db	44448	GCTGGGTGTGGCATGCACTGTGATCTCTAGTCTACTCGGAGAGGCTGAGGTGAGGGTGA	44389
QY	2761	TTGCTTTGAGCCAGGAGTTGAGGCTGCACTGAGCAGCATGCTGTGCCACTGTACTTTCCAG	2820
Db	44388	TTGCTTTGAGCCAGGAGTTGAGGCTGCACTGAGCAGCATGCTGTGCCACTGTACTTTCCAG	44329
QY	2821	CTAGGTGACAGACAGACCCCTGTCTCCCTGACCCCTCGAAAAAGAGAGATTTAAAGT	2880
Db	44328	CTAGGTGACAGACAGACCCCTGTCTCCCTGACCCCTCGAAAAAGAGAGATTTAAAGT	44269
QY	2881	TGACCTTTGTTCTTTATTTTAAATTTTGGCTGTAGCAGTGGGTAAATTTGGCAATGCCAT	2940
Db	44268	TGACCTTTGTTCTTTATTTTAAATTTTGGCTGTAGCAGTGGGTAAATTTGGCAATGCCAT	44209
QY	2941	TTCTCAGATGGTGAAGGAGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTCGCATTTG	3000
Db	44208	TTCTCAGATGGTGAAGGAGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTCGCATTTG	44150
QY	3001	GGACATGTTAAAGTGTGAGATTTCCAGTCCAGGCTTCAAGTGGTGGGCCACATAGGCAGTT	3060
Db	44149	GGACATGTTAAAGTGTGAGATTTCCAGTCCAGGCTTCAAGTGGTGGGCCACATAGGCAGTT	44090
QY	3061	CAGTGTAGAAATTCAGGACCAAGGCTGGGACGCGTGGTCTCACTCTGTAAATCCCAGCACT	3120
Db	44089	CAGTGTAGAAATTCAGGACCAAGGCTGGGACGCGTGGTCTCACTCTGTAAATCCCAGCACT	44030
QY	3121	TTGTTGGCTGAGCGAGGTAGATCATTTGAGGTTCAGAGTTTCAGACAACGCTTTGGCCAA	3180
Db	44029	TTGTTGGCTGAGCGAGGTAGATCATTTGAGGTTCAGAGTTTCAGACAACGCTTTGGCCAA	43970
QY	3181	TGTTGAAACCCCATGTCTACTAAAAATACAAAAATTTAGCTGTGTGTGGGCGCAGCCT	3240
Db	43969	TGTTGAAACCCCATGTCTACTAAAAATACAAAAATTTAGCTGTGTGTGGGCGCAGCCT	43910
QY	3241	ATAGTCCCAAGGTTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTTGAAACCCAGGAGGTGCAGG	3300
Db	43909	ATAGTCCCAAGGTTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTTGAAACCCAGGAGGTGCAGG	43850
QY	3301	TTGCGAGTGAAGTGTGCGCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTCT	3360
Db	43849	TTGCGAGTGAAGTGTGCGCACTGCACTCCAGCCTGGGTGATAGAGTGAGACTCTCT	43790
QY	3361	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	3420
Db	43789	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	43730
QY	3421	TCTAAATTTGCTGAGCACCACCTCCTGAGTTCAAATACATGGGTAGACACACCTTTAAC	3480
Db	43729	TCTAAATTTGCTGAGCACCACCTCCTGAGTTCAAATACATGGGTAGACACACCTTTAAC	43670
QY	3481	ATTTTCTAGATCCACAGCTTTTAGTGGAGTCTGTCTAATCATGATGATTTGGAAATAGGAT	3540
Db	43669	ATTTTCTAGATCCACAGCTTTTAGTGGAGTCTGTCTAATCATGATGATTTGGAAATAGGAT	43610
QY	3541	CTGGGGGAGTGGAGGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAGGAAAGAGC	3600
Db	43609	CTGGGGGAGTGGAGGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAGGAAAGAGC	43550
QY	3601	ACCCAGGAGTGTATATGGAAGAAAGACAGGAGCTCACTACCTTTCAAAAAATGAGGA	3660

Db 43549 ACCCAGGACTGTTCATATGGAAGAAAGACAGGACTGCAACTCACCCTTACAAAAATGAGGA 43490
QY 3661 CCAGACACAGCTGATGGTATAGTTGATGACAGGTGTGTGGAGCCTCAACATCCTCTCC 3720
Db 43489 CCAGACACAGCTGATGGTATAGTTGATGACAGGTGTGTGGAGCCTCAACATCCTCTCC 43430
QY 3721 CTCCTACTACACATGGTTAAGCCCTGTGCTCTGCTCCAGGTTACACACTCTCTGCACTA 3780
Db 43429 CTCCTACTACACATGGTTAAGCCCTGTGCTCTGCTCCAGGTTACACACTCTCTGCACTA 43370
QY 3781 CCTCTTCATGGGTGCTCTCAGACAGGACCTTGGTCTTTCCTTGTGTAAGCTTTGGGCTA 3840
Db 43369 CCTCTTCATGGGTGCTCTCAGACAGGACCTTGGTCTTTCCTTGTGTAAGCTTTGGGCTA 43310
QY 3841 CGTGATGACACAGCTGTGCTTCTATGATCATGAGAGTCCCGTGTGGAGCCCGGAAC 3900
Db 43309 CGTGATGACACAGCTGTGCTTCTATGATCATGAGAGTCCCGTGTGGAGCCCGGAAC 43250
QY 3901 TCCATGGGTTCACAGTAGAATTTCAAGCCAGATGTGGCTGCAAGTCTGAGTCTGAA 3960
Db 43249 TCCATGGGTTCACAGTAGAATTTCAAGCCAGATGTGGCTGCAAGTCTGAGTCTGAA 43190
QY 3961 AGGGTGGATACATGTTTCACTGTGTGACTTCTGGACTATTTATGAAAAATCAACACACAG 4020
Db 43189 AGGGTGGATACATGTTTCACTGTGTGACTTCTGGACTATTTATGAAAAATCAACACACAG 43130
QY 4021 CAAGGGTATGTGGAGGGGGCTCACCTTCTCTGAGGTTGTGAGAGCTTTTCACTTTTC 4080
Db 43129 CAAGGGTATGTGGAGGGGGCTCACCTTCTCTGAGGTTGTGAGAGCTTTTCACTTTTC 43070
QY 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGAGCAGGAGAGGGAAG 4140
Db 43069 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGAGCAGGAGAGGGAAG 43010
QY 4141 GAATTTGCTTCTCGAGATCAATTTGCTTCTGGGATGTGGAAATAGGACCTATTCTTT 4200
Db 43009 GAATTTGCTTCTCGAGATCAATTTGCTTCTGGGATGTGGAAATAGGACCTATTCTTT 42950
QY 4201 TGGTTGCAGTTAAACAGGCTGGGATTTTTTCAGAGTCCACACCCCTGCAAGTCACTCTG 4260
Db 42949 TGGTTGCAGTTAAACAGGCTGGGATTTTTTCAGAGTCCACACCCCTGCAAGTCACTCTG 42890
QY 4261 GCCTGTGAAATGCAAGAGACAAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGG 4320
Db 42889 GCCTGTGAAATGCAAGAGACAAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGG 42830
QY 4321 CAGGACCACTTTGAATTTCTGCCCTGCACACACTGGATTGGAGAGCAGAGAACCCAGGGCC 4380
Db 42829 CAGGACCACTTTGAATTTCTGCCCTGCACACACTGGATTGGAGAGCAGAGAACCCAGGGCC 42770
QY 4381 TGGCCCAACAGCTGGAGTGGGAAAGGCAAGATTCGGGCCAGGAGGAGGAGGAGGAGGAGG 4440
Db 42769 TGGCCCAACAGCTGGAGTGGGAAAGGCAAGATTCGGGCCAGGAGGAGGAGGAGGAGGAGG 42710
QY 4441 CTGGAGAGGAGTGCCTGCACAGCTGCAGAGTGTGAGAGTGTGGAGTGTGGAGTGTGGAG 4500
Db 42709 CTGGAGAGGAGTGCCTGCACAGCTGCAGAGTGTGAGAGTGTGGAGTGTGGAGTGTGGAG 42650
QY 4501 GACCAACAGGATGAGTGGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
Db 42649 GACCAACAGGATGAGTGGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 42590
QY 4561 AGGTTGCAGGGACAGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620
Db 42589 AGGTTGCAGGGACAGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 42530
QY 4621 TCCAAATTCGGGAAGGAGCTTTCTCAATCCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680
Db 42529 TCCAAATTCGGGAAGGAGCTTTCTCAATCCTAGAGTCTCTACCTTATAATTTGAGATGTA 42470
QY 4681 TGAGACAGCCACAGTCAATGGGTTTAAATTTCTTTTCTCCATGATATGGCTCAAAAGGAA 4740
Db 42469 TGAGACAGCCACAGTCAATGGGTTTAAATTTCTTTTCTCCATGATATGGCTCAAAAGGAA 42410

QY 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA 4800
Db 42409 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA 42350
QY 4801 AAATTCAGAAATGTCAAGGCCGGGACGGTGGCTCACCCCTGTAATCCAGCACCTTTGGG 4860
Db 42349 AAATTCAGAAATGTCAAGGCCGGGACGGTGGCTCACCCCTGTAATCCAGCACCTTTGGG 42290
QY 4861 AGGCCGAGCGGGTGGTCAAGGCTCAGAGTCTTGGAGCCAGCCTGACCAACATCGTGAA 4920
Db 42289 AGGCCGAGCGGGTGGTCAAGGCTCAGAGTCTTGGAGCCAGCCTGACCAACATCGTGAA 42230
QY 4921 ACCCGTCTCTAAAAAATACAAAAATTAGCTGGTGCATGATGCGCACCTGTAGTCCCA 4980
Db 42229 ACCCGTCTCTAAAAAATACAAAAATTAGCTGGTGCATGATGCGCACCTGTAGTCCCA 42170
QY 4981 GCTAATTCGAAGGCTGAGGC 5000
Db 42169 GCTAATTCGAAGGCTGAGGC 42150

RESULT 12
AAA96794
ID AAA96794 standard; cDNA; 12146 BP.
XX
AC AAA96794;
XX
DT 19-FEB-2001 (first entry)
XX
DE Genomic DNA of a histocompatibility iron loading (HFE) gene.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 1028..1324
FT /tag= a
FT /number= 1
FT intron 1325..4651
FT /tag= b
FT /number= 1
FT exon 4652..4915
FT /tag= c
FT /number= 2
FT intron 4916..5124
FT /tag= d
FT /number= 2
FT exon 5125..5400
FT /tag= e
FT /number= 3
FT intron 5401..6493
FT /tag= f
FT /number= 3
FT exon 6494..6769
FT /tag= g
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FT intron 6770..6927
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FT /number= 4
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FT exon 7995..9050
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FT /number= 6
FT intron 9051..10205

FT exon /*tag= 1 /number= 6 /tag= m 10206..10637

FT exon WO200058515-A1.

FT exon 05-OCT-2000.

FT exon 24-MAR-2000; 2000WO-US007982.

FT exon 26-MAR-1999; 99US-00277457.

FT exon (BILL-) BILLUPS-ROTHENBERG INC.

FT exon Rothenberg BE, Sawada-Hirai R, Barton JC;

FT exon WPI; 2000-647244/62.

FT exon Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid.

FT exon Example 1; Page 21-28; 55pp; English.

FT exon The present sequence represents the human histocompatibility iron loading (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in CC A96769 (Genbank Accession number U60319). The presence of the mutation CC indicates the disorder or the genetic susceptibility to the disorder. The CC method is used to diagnose an iron disorder e.g. haemochromatosis, or a CC genetic susceptibility to develop it

FT exon SQ Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 U; 0 Other;

FT exon Query Match 99.1%; Score 4957.2; DB 3; Length 12146;

FT exon Best Local Similarity 99.8%; Pred. No. 0;

FT exon Matches 4995; Conservative 0; Mismatches 3; Indels 6; Gaps 3;

QY 1 TCTAAGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATATAATTTA 60

DB 889 TCTAAGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATATAATTTA 948

QY 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACCCCT 120

DB 949 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACCCCT 1008

QY 121 TCAGGTTTAAACCAAGGGGACACTGGATCAGTGTGTTTCAAGGAGGTACCTT 180

DB 1009 TCAGGTTTAAACCAAGGGGACACTGGATCAGTGTGTTTCAAGGAGGTACCTT 1068

QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAGACCTGTTGCTTTTCCACGAGGAT 240

DB 1069 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAGACCTGTTGCTTTTCCACGAGGAT 1128

QY 241 TTACTGGGATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 300

DB 1129 TTACTGGGATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 1188

QY 301 TTTCCCGCCCAAAAGAGCGGAGATTAAACGGGACGTGCGGCGAGAGCTGGGAA 360

DB 1189 TTTCCCGCCCAAAAGAGCGGAGATTAAACGGGACGTGCGGCGAGAGCTGGGAA 1248

QY 361 ATGGGCGCCGAGCCAGGCGGCTTCTCCTGATGCTTTTGAGACCGCGGTCCTG 420

DB 1249 ATGGGCGCCGAGCCAGGCGGCTTCTCCTGATGCTTTTGAGACCGCGGTCCTG 1308

QY 421 CAGGGCGCTTGCTGCTGAGTCCGAGGGCTGCGGCGAACTAGGGCGCGCGGGGTG 480

DB 1309 CAGGGCGCTTGCTGCTGAGTCCGAGGGCTGCGGCGCAACTAGGGCGCGGGGTG 1368

QY 481 GAAAAATCGAAATAGCTTTTCTTTCGCTGGAGTTTGTCTAACTTTGGAGGAGCTGC 540

DB 1369 GAAAAATCGAAATAGCTTTTCTTTCGCTGGAGTTTGTCTAACTTTGGAGGAGCTGC 1428

QY 541 TCAACCCCTATCCGCAAGCCCTCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 600

DB 1429 TCAACCCCTATCCGCAAGCCCTCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 1488

QY 601 CTACCACTGAATGCGAGATAGGGTCTCTCGGCCCCAGGACCTGCCCTCCCCCGCTGT 660

DB 1489 CTACCACTGAATGCGAGATAGGGTCTCTCGGCCCCAGGACCTGCCCTCCCCCGCTGT 1548

QY 661 CCGGGCTCTGCGAGTACTTTTGGNACCGCCCACTCCCTTCCCTCCCAACTAGNATGCTTT 720

DB 1549 CCGGGCTCTGCGAGTACTTTTGGNACCGCCCACTCCCTTCCCTCCCAACTAGNATGCTTT 1608

QY 721 TAAATAAATCTCGTAGTTCTCTCACTTGAGCTAGGCTAAGCCTGGGGCTCTCTTGAACCTGG 780

DB 1609 TAAATAAATCTCGTAGTTCTCTCACTTGAGCTAGGCTAAGCCTGGGGCTCTCTTGAACCTGG 1668

QY 781 AACTCGGGTTTATTTCCAAATGCTGTGCAAGTTTTCCTCCAGTCATCTCCAAACAGG 840

DB 1669 AACTCGGGTTTATTTCCAAATGCTGTGCAAGTTTTCCTCCAGTCATCTCCAAACAGG 1728

QY 841 AAGTTCTTCCCTGAGTCTTCCGAGAGAGCTGAGCAAAACCCACAGCAGATCCGACCG 900

DB 1729 AAGTTCTTCCCTGAGTCTTCCGAGAGAGCTGAGCAAAACCCACAGCAGATCCGACCG 1788

QY 901 GGTTTCCACCTCAGAACCAATCGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGGA 960

DB 1789 GGTTTCCACCTCAGAACCAATCGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGGA 1848

QY 961 TCTGAATTTTCCACCTTCCACCTTTCCTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020

DB 1849 TCTGAATTTTCCACCTTTCCTGAGACCTGGGGTGGAGGTCTCTAGGGT 1908

QY 1021 GGGAGCTCTGAGAGAGCCCTACCTCGGGCCCTTTCCCACTCTTGGCAATGTTCTTTT 1080

DB 1909 GGGAGCTCTGAGAGAGCCCTACCTCGGGCCCTTTCCCACTCTTGGCAATGTTCTTTT 1968

QY 1081 GCCTCGAAAAATTAAGTATATGTTAGTTTGAACCTTGAACCTGAACTCTCTTTTCGG 1140

DB 1969 GCCTCGAAAAATTAAGTATATGTTAGTTTGAACCTTGAACCTGAACTCTCTTTTCGG 2028

QY 1141 CTAGGCTTTATGATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTCAAAAGTACTGA 1200

DB 2029 CTAGGCTTTATGATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTCAAAAGTACTGA 2088

QY 1201 TAATGAACATGTAAGCAATGCACTCACTTAAGTTTACATTCATCTCATCTTATTTCA 1260

DB 2089 TAATGAACATGTAAGCAATGCACTCACTTAAGTTTACATTCATCTCATCTTATTTGA 2148

QY 1261 TTTTTCATAGGATAGGAGGTAGGAGCTAAATACTGTTTATTTTACTAGAAGTTAACT 1320

DB 2149 TTTTTCATAGGATAGGAGGTAGGAGCTAAATACTGTTTATTTTACTAGAAGTTAACT 2208

QY 1321 GGAATTCAGATTTATTAATCTTTTTCAGGTTCACAAAGAACATAAATAATCTGGTTCTCG 1380

DB 2209 GGAATTCAGATTTATATACTCTTTTCAGGTTCACAAAGAACATAAATAATCTGGTTCTCG 2268

QY 1381 ATGTTATTTCAAGTACTACAGTCTTCTTAATCTTAGTTGACAGTATTTTCCCTCTGATG 1440

DB 2269 ATGTTATTTCAAGTACTACAGTCTTCTTAATCTTAGTTGACAGTATTTTCCCTCTGATG 2328

QY 1441 TGTAGCAGAGTCTCTGTTGGGTCAACCGCGGCTCAGCAGCAGCTTTGAGTTTGGTA 1500

DB 2329 TGTAGCAGAGTCTCTGTTGGGTCAACCGCGGCTCAGCAGCAGCTTTGAGTTTGGTA 2388

QY 1501 CTACGCTGATCCACATTTTACATGACAAAGATGAGGCATGCGCAGCGCTCTCTCTG 1560

Qy	2101	CCTCCCTACTACTCCTAGTGTCTAGAGGACATCCCCCACTCTTGACAAACCAAAAATGTCTCT	2160
Db	45002	CCTCCCTACTACTCCTAGTGTCTAGAGGACATCCCCCACTCTTGACAAACCAAAAATGTCTCT	44943
Qy	2161	AAACTTTGGCCACATGTCACTCTAGTAGACAAATCCTCGTTTAAAGAGCTCGGGTTCAAAA	2220
Db	44942	AAACTTTGCCACATGTCACTCTAGTAGACAAATCCTCGTTTAAAGAGCTCGGGTTCAAAA	44883
Qy	2221	AATAAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA	2280
Db	44882	AATAAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAGAGGA	44823
Qy	2281	GCCACAAACAAGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATCTCTAGCCAAAGGATG	2340
Db	44822	GCCACAAACAAGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATCTCTAGCCAAAGGATG	44763
Qy	2341	ACAGTGATCTGTCAACAGGCTTTTTAAAGATTGCTCTCGGCTGCTATGTGGAAGACGAATG	2400
Db	44762	ACAGTGATCTGTCAACAGGCTTTTTAAAGATTGCTCTCGGCTGCTATGTGGAAGACGAATG	44703
Qy	2401	AAGGGAGCAACAGTAAAGCAGGAGCCCAAGCAGGAAGCTGTTCACAGTCCAGGCAAG	2460
Db	44702	AAGGGAGCAACAGTAAAGCAGGAGCCCAAGCAGGAAGCTGTTCACAGTCCAGGCAAG	44643
Qy	2461	AGTGTGTGAGTGGGCTGGGTGGGAACAGAAAGAGGAGTGAACAACATGTCTCTGAA	2520
Db	44642	AGTGTGTGAGTGGGCTGGGTGGGAACAGAAAGAGGAGTGAACAACATGTCTCTGAA	44583
Qy	2521	TATATCTGAAGAGAGTTGCTGAAGATTTCTATGTTGTGTGAGAGAAAGAGAGAAATTTGG	2580
Db	44582	TATATCTGAAGAGAGTTGCTGAAGATTTCTATGTTGTGTGAGAGAAAGAGAGAAATTTGG	44523
Qy	2581	CTGGGTGTAGTGTCAATGCAAGAGGAGGCGCCAAGCAGAGCAGATTTCTCTGAGCTCAGGA	2640
Db	44522	CTGGGTGTAGTGTCAATGCAAGAGGAGGCGCCAAGCAGAGCAGATTTCTCTGAGCTCAGGA	44463
Qy	2641	GTTCAAGACCAAGCCTGGGCAACAACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
Db	44462	GTTCAAGACCAAGCCTGGGCAACAACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	44403
Qy	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCTCTAGCTACTCGGAGGCTCAGGTGGAGGTA	2760
Db	44402	GCTGGGTGTGGTGGCATGCACCTGTGATCTCTAGCTACTCGGAGGCTCAGGTGGAGGTA	44343
Qy	2761	TTGCTTGAGCCCAAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCACTGTACTTTCAGC	2820
Db	44342	TTGCTTGAGCCCAAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCACTGTACTTTCAGC	44283
Qy	2821	CTAGGTGACAGACAGACCCCTGTCTCCCTGCACCCCTGAAAAAGAGAGAGTTAAAGT	2880
Db	44282	CTAGGTGACAGACAGACCCCTGTCTCCCTGCACCCCTGAAAAAGAGAGAGTTAAAGT	44223
Qy	2881	TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAAATTGGCAATGCCAT	2940
Db	44222	TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAAATTGGCAATGCCAT	44163
Qy	2941	TTCTGAGATCGGTCAAGCAGAGGAAAGACAGTTTGGGGTAAATCAAGATCTCGCATTTG	3000
Db	44162	TTCTGAGATCGGTCAAGCAGAGGAAAGACAGTTTGGGGTAAATCAAGATCTCGCATTTG	44104
Qy	3001	GGACATGTTTAAAGTTTGAGATTTCCAGTTCAGGCTTCCAAGTGTGGGCGCACATAGGCAGTT	3060
Db	44103	GGACATGTTTAAAGTTTGAGATTTCCAGTTCAGGCTTCCAAGTGTGGGCGCACATAGGCAGTT	44044
Qy	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCAAGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Db	44043	CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCAAGGTGGCTCACTTCTGTAAATCCAGCACT	43984
Qy	3121	TTGGTGGCTCAGGCGAGTATCATTTGAGTTCAGGAGTTTCAGACACAGCTTGGCACAACA	3180
Db	43983	TTGGTGGCTCAGGCGAGTATCATTTGAGTTCAGGAGTTTCAGACACAGCTTGGCACAACA	43924
Qy	3181	TGGTGAACCCCAATGTCTACTAAAAATACAAAAATTTAGCCTCGGTGTGGTGGCGCACGCT	3240

[illegible]

Db 42843 CCTGGGCTGTGAATGCAAGACAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGA 42784
 QY 4317 TGGGAGGACCACTTGAATTCGCTCGACACACTGGAATGGAGAGCAGAACCCAG 4376
 Db 42783 TGGGAGGACCACTTGAATTCGCTCGACACACTGGAATGGAGAGCAGAACCCAG 42724
 QY 4377 GGCCTGGCCCAACAGCTGGAGTGGGAAGGCACAGATTCGGGCCAGGCAGACAGGC 4436
 Db 42723 GGCCTGGCCCAACAGCTGGAGTGGGAAGGCACAGATTCGGGCCAGGCAGACAGGC 42664
 QY 4437 CTACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGT 4496
 Db 42663 CTACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGT 42604
 QY 4497 TTTGACCAACAGGTATGGTGGAAACACACTTTCGCCCTATATCTCTAGTGGCAGAGTG 4556
 Db 42603 TTTGACCAACAGGTATGGTGGAAACACACTTTCGCCCTATATCTCTAGTGGCAGAGTG 42544
 QY 4557 GAGGAGGTTCAGGGCAGCGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTG 4616
 Db 42543 GAGGAGGTTCAGGGCAGCGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTG 42484
 QY 4617 CCTCTCCAAATTCCTGGGAGGAGCTTCTCAATCCTAGAGTCTCTACCTTATATTTGAGA 4676
 Db 42483 CCTCTCCAAATTCCTGGGAGGAGCTTCTCAATCCTAGAGTCTCTACCTTATATTTGAGA 42424
 QY 4677 TGTATGAGACGCCACAAGTCAATGAGTTAATTTCTTTTCCATGCAATATGCTCAAAAG 4736
 Db 42423 TGTATGAGACGCCACAAGTCAATGAGTTAATTTCTTTTCCATGCAATATGCTCAAAAG 42364
 QY 4737 GGAAGTGTATGCGCCCTGCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTG 4796
 Db 42363 GGAAGTGTATGCGCCCTGCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTG 42304
 QY 4797 TTAAAAATTCAGAAATGTCAAGCCCGGCACAGGTGGCTCACCCCTGTATATCCAGCACTT 4856
 Db 42303 TTAAAAATTCAGAAATGTCAAGCCCGGCACAGGTGGCTCACCCCTGTATATCCAGCACTT 42244
 QY 4857 TGGGAGGCGGAGGCGGGTGGTCAAGGTCAAGGTTCAGACACAGCTGACCAACATGG 4916
 Db 42243 TGGGAGGCGGAGGCGGGTGGTCAAGGTCAAGGTTCAGACACAGCTGACCAACATGG 42184
 QY 4917 TGAAACCCGCTCTTAAAAAATACAAAAAATAGCTGGTCACAGTCATCGCACCTGTAGT 4976
 Db 42183 TGAAACCCGCTCTTAAAAAATACAAAAAATAGCTGGTCACAGTCATCGCACCTGTAGT 42124
 QY 4977 CCCAGCTAATTGGAAGGCTGAGGC 5000
 Db 42123 CCCAGCTAATTGGAAGGCTGAGGC 42100

RESULT 14

ABV93934

ID ABV93934 standard; DNA; 5982 BP.

XX AC ABV93934;

XX 08-JAN-2003 (first entry)

XX Human colon specific nucleic acid, SEQ ID 25.

XX Human; colon; cytostatic; vaccine; gene therapy; colon cancer;

XX KW colon disorder; metastasis; ds.

XX OS Homo sapiens.

XX PN WO200277234-A2.

XX 03-OCT-2002.

XX 31-OCT-2001; 2001WO-US048414.

XX 31-OCT-2000; 2000US-0244759P.

XX (DIAD-) DIADEXUS INC.
 PA Sun Y, Recipon H, Ghosh MG, Liu C;
 XX WPI; 2003-018928/01.
 DR
 XX New isolated colon-specific nucleic acid molecule, useful for treating
 PT colon cancer, and diagnosing or monitoring the presence of metastases of
 PT colon cancer in a patient.
 XX
 PS Claim 1; Page 155-156; 216pp; English.
 XX
 CC The present invention relates to human colon specific nucleic acids
 CC (ABV93910-ABV94009) and proteins (ABP68360-ABP68435). The nucleic acids
 CC and proteins are useful for treating colon cancer and colon disorders,
 CC and diagnosing or monitoring the presence of colon disorders and
 CC metastases of colon cancer in a patient
 XX
 SQ Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 0 U; 2 Other;

Query Match 92.2%; Score 4607.8; DB 8; Length 5982;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 4628; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 361 ATGGGCGCGCAGCAGCCGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 420
 Db 1 ATGGGCGCGCAGCAGCCGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 60
 QY 421 CAGGGGCGCTTGTCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 480
 Db 61 CAGGGGCGCTTGTCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 120
 QY 481 GAAAAATCGAAATAGCTTTTCTTGGCTTGGAGTTTCTAACTTTGAGAGCACTGC 540
 Db 121 GAAAAATCGAAATAGCTTTTCTTGGCTTGGAGTTTCTAACTTTGAGAGCACTGC 180
 QY 541 TCAACCTATCCGAAAGCCCTCTCCCTACTTTCTGGCTCCAGACCCCGTCCAGAGGAGTGC 600
 Db 181 TCAACCTATCCGAAAGCCCTCTCCCTACTTTCTGGCTCCAGACCCCGTCCAGAGGAGTGC 240
 QY 601 CTACACTGAACTCAGATAGGGGTCTCTCCCTCCAGACCTGCCCCCTCCCGGCTGT 660
 Db 241 CTACACTGAACTCAGATAGGGGTCTCTCCCTCCAGACCTGCCCCCTCCCGGCTGT 300
 QY 661 CCCGGCTCTGGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGATGCTTT 720
 Db 301 CCCGGCTCTGGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGATGCTTT 360
 QY 721 TAAATAATCTCTAGTTCTCTCACTGAGCTGAGCTAAGCTGGGGCTCTTGAACCTGG 780
 Db 361 TAAATAATCTCTAGTTCTCTCACTGAGCTGAGCTAAGCTGGGGCTCTTGAACCTGG 420
 QY 781 AACTCGGGTTTATTTTCAATGTGAGCTGTGAGTTTTTTTCCCAAGTCACTCTCCAAACAGG 840
 Db 421 AACTCGGGTTTATTTTCAATGTGAGCTGTGAGTTTTTTTCCCAAGTCACTCTCCAAACAGG 480
 QY 841 AAGTTCTTCTCTGAGTGTCTCCGAGAGGCTGAGCAAAACCAACAGAGGATCCGACAGG 900
 Db 481 AAGTTCTTCTCTGAGTGTCTCCGAGAGGCTGAGCAAAACCAACAGAGGATCCGACAGG 540
 QY 901 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGGGAAGAGTGGCGTTGGGGA 960
 Db 541 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGGGAAGAGTGGCGTTGGGGA 600
 QY 961 TCTGAATTTCTTCAACATTTCCACCTTTTGGTGAGACTCTGGGTGGAGGTCTCTAGGGT 1020
 Db 601 TCTGAATTTCTTCAACATTTCCACCTTTTGGTGAGACTCTGGGTGGAGGTCTCTAGGGT 660
 QY 1021 GGGAGGCTCTTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTGGCAATGTTCTTTT 1080
 Db 661 GGGAGGCTCTTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTGGCAATGTTCTTTT 720

Qy	1081	GCCTGGAAAAATTAAGTATATGTTAGTTTGGAACTGGAACAAATTCCTCTTTTCGG	1141
Db	721	GCCTGGAAAAATTAAGTATATGTTAGTTTGGAACTGGAACAAATTCCTCTTTTCGG	780
Qy	1141	CTAGGCTTTATTTGATTTTGCAATGTGCTGTAAATTAAGAGGCCCTCTCAACAAGTACTGA	1200
Db	781	CTAGGCTTTATTTGATTTTGCAATGTGCTGTAAATTAAGAGGCCCTCTCAACAAGTACTGA	840
Qy	1201	TAATGAACATGTAAGCAATGCACCTCACCTCTTAAGTTACATTCATATCTGATCTTATTTGA	1260
Db	841	TAATGAACATGTAAGCAATGCACCTCACCTCTTAAGTTACATTCATATCTGATCTTATTTGA	900
Qy	1261	TTTTCTAGGCATAGGAGGTAGGAGCTAAATAATAGCTTTTATTTTACTAGAGTTAACT	1320
Db	901	TTTTCTAGGCATAGGAGGTAGGAGCTAAATAATAGCTTTTATTTTACTAGAGTTAACT	960
Qy	1321	GGAAATTCAGATTATATAACTCTTTTCAGGTTTACAAAGAACATAAATACTGTGTTTCTG	1380
Db	961	GGAAATTCAGATTATATAACTCTTTTCAGGTTTACAAAGAACATAAATACTGTGTTTCTG	1020
Qy	1381	ATGTTATTTCAAGTACTACAGCTGCTTCTTAATCTTAGTTGACAGTGATTTTGCCCTGTAG	1440
Db	1021	ATGTTATTTCAAGTACTACAGCTGCTTCTTAATCTTAGTTGACAGTGATTTTGCCCTGTAG	1080
Qy	1441	TGTAGCACAGTGTCTGTGGGTACACGCCGCCCTCAGCACAGCACTTTGAGTTTTGGTTA	1500
Db	1081	TGTAGCACAGTGTCTGTGGGTACACGCCGCCCTCAGCACAGCACTTTGAGTTTTGGTTA	1140
Qy	1501	CTACGTGTATCCACATTTTACACATGACAAAGATGAGGCATGCCAGGCCGTCTCTCTGG	1560
Db	1141	CTACGTGTATCCACATTTTACACATGACAAAGATGAGGCATGCCAGGCCGTCTCTCTGG	1200
Qy	1561	CAAAATTTATTCAAATGTTACACTGGCTTTGGTGGCAGAGCTCATGTCTCCACATTCATAGC	1620
Db	1201	CAAAATTTATTCAAATGTTACACTGGCTTTGGTGGCAGAGCTCATGTCTCCACATTCATAGC	1260
Qy	1621	TATGATTTCTTAAACATCACACTGCAATGAGGTTGAAATAAATAATTCATGTGAGCAG	1680
Db	1261	TATGATTTCTTAAACATCACACTGCAATGAGGTTGAAATAAATAATTCATGTGAGCAG	1320
Qy	1681	AAATATTTCAATGTTTACAAGTGTAAATGAGTCCCGCCAGCATGTGTGCACHTGTTCAAGCCC	1740
Db	1321	AAATATTTCAATGTTTACAAGTGTAAATGAGTCCCGCCAGCATGTGTGTGCACHTGTTCAAGCCC	1380
Qy	1741	CAAGGAGAGAGCAGGGAACAAAGTCTTTTACCCTTTTGATATTTTGTCAATCTAGTGGAGA	1800
Db	1381	CAAGGAGAGAGCAGGGAACAAAGTCTTTTACCCTTTTGATATTTTGTCAATCTAGTGGAGA	1440
Qy	1801	GATGACAAATTAAGCAAAATGACAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA	1860
Db	1441	GATGACAAATTAAGCAAAATGACAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA	1500
Qy	1861	GNAGCAGAGAAGTCAGGGCAAGTCACCTCGGGCTGACACTTGACGACAGACATGAAGGA	1920
Db	1501	GNAGCAGAGAAGTCAGGGCAAGTCACCTCGGGCTGACACTTGACGACAGACATGAAGGA	1560
Qy	1921	AATAAGAAATGATATTGATCTGGAGCAGTATTTCCAGGGCAAACTGAGTGGCCCTGCCAAG	1980
Db	1561	AATAAGAAATGATATTGATCTGGAGCAGTATTTCCAGGGCAAACTGAGTGGCCCTGCCAAG	1620
Qy	1981	TTTGATTTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG	2040
Db	1621	TTTGATTTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG	1680
Qy	2041	CGGGCTGGGGTGGGAAGGGGGACTACCATCTGATGTAGGATGTCTAGCAGTATCCTGT	2100
Db	1681	CGGGCTGGGGTGGGAAGGGGGACTACCATCTGATGTAGGATGTCTAGCAGTATCCTGT	1740
Qy	2101	CCTCCCTACTTCACTTAGTGTCTAGGACACTCCCCAGTCTTGTGACACCAAAAATGCTCT	2160
Db	1741	CCTCCCTACTTCACTTAGTGTCTAGGACACTCCCCAGTCTTGTGACACCAAAAATGCTCT	1800
Qy	2161	AAACTTTTGCCACATGTCACTCTAGTAGACAAACTCCTGGTTTAAAGAGCTCGGTTGAAAAA	2220

1801	DB	AAA	CTTTGCCACATGTCACCTAGTACAACTCCTGGTTAAGAAAGCTCGGTTGTA	1860
2221	QY	AATAAA	CAAGTAGTCTGGGAGGTAGAGGCCAAGAGTAGTAAATGGGCTCAGACAGGA	2280
1861	DB	AATAAA	CAAGTAGTCTGGGAGGTAGAGGCCAAGAGTAGTAAATGGGCTCAGACAGGA	1920
2281	QY	GCCAAA	CAAGTTGTGCAGGGCCCTGTAGGCTGTGGTGTGAATTTAGCCAAAGAGTA	2340
1921	DB	GCCAAA	CAAGTTGTGCAGGGCCCTGTAGGCTGTGGTGTGAATTTAGCCAAAGAGTA	1980
2341	QY	ACAGTGAT	CTGTCTCAGGCTTTTAAAGATTGCTCTGGCTGCTATGTGGAAGACGAATG	2400
1981	DB	ACAGTGAT	CTGTCTCAGGCTTTTAAAGATTGCTCTGGCTGCTATGTGGAAGACGAATG	2040
2401	QY	AAGGAGCA	ACAGTAAAGCAGGAGCCAGCCAGCAAGAGCTGTTACACAGTCAGAGCAAG	2460
2041	DB	AAGGAGCA	ACAGTAAAGCAGGAGCCAGCCAGCAAGAGCTGTTACACAGTCAGAGCAAG	2100
2461	QY	AGGTAGTGA	GTGGCTGGGTGGGAAACAGAAAAAGGAGTGACAAACCATTTGCTCTGAA	2520
2101	DB	AGGTAGTGA	GTGGCTGGGTGGGAAACAGAAAAAGGAGTGACAAACCATTTGCTCTGAA	2160
2521	QY	TATATTCTGA	AGGAAGTTGCTGAAGGATTTCTATTGTTGTGAGAGAAAGAGAATTTGG	2580
2161	DB	TATATTCTGA	AGGAAGTTGCTGAAGGATTTCTATTGTTGTGAGAGAAAGAGAATTTGG	2220
2581	QY	CTGGGTGTAG	TAGTCTCATGCCAAGGAGGAGCCCAAGGAGAGCAGATTCCTGAGCTCAGCA	2640
2221	DB	CTGGGTGTAG	TAGTCTCATGCCAAGGAGGAGCCCAAGGAGAGCAGATTCCTGAGCTCAGCA	2280
2641	QY	GTTCAAGA	CACAGCCTGGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA	2700
2281	DB	GTTCAAGC	CAGCCTGGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA	2340
2701	QY	GCTGGGTGTGG	TGCATGCACCTGTGATCTTAGTCTACCTCGGAGGCTGAGGTGGAAGGTA	2760
2341	DB	GCTGGGTGTGG	TGCATGCACCTGTGATCTTAGTCTACCTCGGAGGCTGAGGTGGAAGGTA	2400
2761	QY	TTGCTTCAG	CCCGAGGATTTGAGGCTGCAGTGAGCCATGACTGTGCCTACTGTACTTCAGC	2820
2401	DB	TTGCTTCAG	CCCGAGGATTTGAGGCTGCAGTGAGCCATGACTGTGCCTACTGTACTTCAGC	2460
2821	QY	CTAGGTGAC	AGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT	2880
2461	DB	CTAGGTGAC	AGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT	2520
2881	QY	TGACTTTGTTCT	TTTATTTTAAATTTTATTTGCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
2521	DB	TGACTTTGTTCT	TTTATTTTAAATTTTATTTGCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2580
2941	QY	TTCTCAGAT	CGGTGAGGAGGAGGAGGAGGATTTGGGGTAAATCAAGGATCTGCATTTG	3000
2581	DB	TTCTCAGAT	CGGTGAGGAGGAGGAGGAGGATTTGGGGTAAATCAAGGATCTGCATTTG	2640
3001	QY	GGACATGTTA	AGTTTGGAGTTTCCAGTTCAGGCTTCCAAAGTTGGTGAGGCCACATAGGCAGTT	3060
2641	DB	GGACATGTTA	AGTTTGGAGTTTCCAGTTCAGGCTTCCAAAGTTGGTGAGGCCACATAGGCAGTT	2700
3061	QY	CAGTGTAA	GAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTTCTGTAAATCCGACACT	3120
2701	DB	CAGTGTAA	GAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTTCTGTAAATCCGACACT	2760
3121	QY	TTGGTGGCT	GAGGAGGTAGATCATTTGAGGTCAGAGGTTTGAGACCAAGCTTTGGCCAACA	3180
2761	DB	TTGGTGGCT	GAGGAGGTAGATCATTTGAGGTCAGAGGTTTGAGACCAAGCTTTGGCCAACA	2820
3181	QY	TGGTGAAC	CCCCATGCTACTTAAATACAAAAATTTAGGCTCGTGTGGTGGCGCAGCCT	3240
2821	DB	TGGTGAAC	CCCCATGCTACTTAAATACAAAAATTTAGGCTCGTGTGGTGGCGCAGCCT	2880
3241	QY	ATAGTCCC	CAGGTTTTTTCAGGAGGCTTAGTAGGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	3300

PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
XX Claim 1; SEQ ID NO 2115; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
XX Sequence 8622 BP; 2410 A; 100 C; 2013 G; 4099 T; 0 U; 0 Other;
SQ
Query Match 51.1%; Score 2556.4; DB 6; Length 8622;
Best Local Similarity 80.1%; Pred. No. 0;
Matches 3015; Conservative 0; Mismatches 746; Indels 1; Gaps 1;
QY 1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATAAATATTTA 60
DB 4862 TTTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATAAATATTTA 4921
QY 61 AATAATCAAGTTCAGATCAGAACATTCGAGACTTCTCCCAATCAACACCCCT 120
DB 4922 AATAATTAAGTTAGATAGATATTTGCGAAGTTATTTTAAATTAATATATTTT 4981
QY 121 TCAGGATTTAAACCAAGGGGACACTGATCACCTAGTGTTCACAGCAGGACCTT 180
DB 4982 TTAGGATTTAAANATTAAGGGGATATGATATTTAGTGTATTAAGTAGGATTTT 5041
QY 181 CTGCTGAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACGAGGAT 240
DB 5042 TTGTTGAGGAGAGAGAAATAAAGTTTGAAGATTTGTTGTTTATTAAGGAGTT 5101
QY 241 TTAAGGAGATCTCTGAGGCTAGGCAATAGCTGTAGGAGTCTCTGAGGCAATCCCG 300
DB 5102 TTATTCGGTATTTTTCAGTTAGGTAATAGTTGTAGGAGTATTTTGGAGTTATTTTCG 5161
QY 301 TTTCCCGCCCCCAAGAGCGGAGATTAACGGGGACGTCGCGCCAGAGCTGGGAA 360
DB 5162 TTTTTCGTTTAAAGAGCGGAGATTAACGGGGACGTCGCGGTAGAGTTGGGAA 5221
QY 361 ATGGGCGCGGAGCCAGGCGCGCTCTCCTCTGATGCTTTTGAGACCGCGCTCGT 420
DB 5222 ATGGGTTCCGAGTAGTTCGGGCTTTTTCGATGTTTTCGATGCTGCGGTTTG 5281
QY 421 CAGGGCGCTGTCGTCGAGTCCGAGGCTCGGGCGAACTAGGGCGCGCGGGGTG 480
DB 5282 TAGGGCGCTTGTTCGCTGAGTTCGAGGGTTGCGGGCGAATAGGGCGCGCGGGGTG 5341
QY 481 GAAATATCGAACTAGCTTTTTCGCTGCGCTGGGAGTTGCTAACTTTGGAGGCTCG 540
DB 5342 GAAATATCGAAATAGTTTTTCGCTGCGCTGGGAGTTGTTAAATTTGGAGGATTTG 5401
QY 541 TCAACCTATCCCAAGCCCTCTCCTCTGCTCCAGACCCCGCTGAGGAGTGC 600
DB 5402 TTAATTTATTCGTAAGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5461
QY 601 CTACCACTGAAGTTCAGAGTGGGCTCCCTCGCCCCAGGACCTGCCCTCCCGGCTGT 660
DB 5462 TTAATTTGAAATGATAGGGGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 5521

QY 661 CCCGGCTCTGCGAGTGAATTTTGGAAACCGCCACCTCCCTTCCCCCACTAGAAATGCTTT 720
DB 5522 TTCGGTTTTCGGAGTGATTTTGGAAATCGTTTATTTTATTTTATTTTATTTTATTTT 5581
QY 721 TAAATAAATCTCGTAGTCTCTCCTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 780
DB 5582 TAAATAAATTTCTGATTTTATTTGAGTGAAGTTAAAGTTTGGGGTTCGTTTGGGATTTG 5641
QY 781 AACTCGGGTTATTTCCAAATGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAG 840
DB 5642 AACTCGGGTTATTTTAAATGTTAGTGTGTAGTTTATTTTATTTTATTTTATTTTATTT 5701
QY 841 AAGTTCTTCCCTCAGTGTCTGCGGAGAGGCTGAGCAAAACCCACACAGGATCCGACCG 900
DB 5702 AAGTTTTCCTTTCAGTGTCTGCGGAGAGGCTGAGCAAAATTTATAGTAGGATTCGACG 5761
QY 901 GGTTCACCTCAGAAACGAATGCGTTGGCGGTGGGGCGCGGAAAGAGTGCGGCTGGGGA 960
DB 5762 GGTTCATTTTAAAGAACGAATGCGTTGGCGGTGGGGCGCGGAAAGAGTGCGGCTGGGGA 5821
QY 961 TCTGAATTCCTCACCATTCCACCTTTCCTGTCAGCTGTCAGCTGTCAGCTGTCAGCTGTCAG 1020
DB 5822 TTGGAATTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 5881
QY 1021 CGGAGGCTCTCAGAGAGGCTTACCTCGGGCCCTTTCCCCACCTCTTGGCAATTTGCTTTT 1080
DB 5882 GGGAGGTTTTCAGAGAGGCTTATTTTCGGGTTTATTTTATTTTATTTTATTTTATTTT 5941
QY 1081 GCTCGAAATTAAGTATATGTTAGTTTGAACGTTTGAACGTTTGAACGTTTGAACGTTTGA 1140
DB 5942 GTTTCGAAATTAAGTATATGTTAGTTTGAACGTTTGAACGTTTGAACGTTTGAACGTTT 6001
QY 1141 CTAGGCTTTATTTGATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB 6002 TTAGGTTTATTTGATTTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6061
QY 1201 TAATGAACATGTAAGCAATGCTCACTCTTAAGTTTACATTCATATCTCATCTCTATTTGA 1260
DB 6062 TAATGAATATGTAAGTAATGTTATTTTAAAGTTTATTTTATTTTATTTTATTTTATTT 6121
QY 1261 TTTTCACTAGGATAGGAGGAGGCTAAATACGTTTATTTTATTTTATTTTATTTTATTTTATTT 1320
DB 6122 TTTTATTTAGGTAAGGAGGAGGAGGTTAAATACGTTTATTTTATTTTATTTTATTTTATTT 6181
QY 1321 GCAATTCAGATTTATATCTCTTTTCAGGTTTCAAGAACATTAATTAATCTGTTTCTGTTCTG 1380
DB 6182 GCAATTTAGATTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 6241
QY 1381 ATGTTTATTTCAAGTACTACAGCTGCTTCTAAATCTTGTAGTTGACAGTATTTTGGCCCTGTAG 1440
DB 6242 ATGTTTATTTTAAATATATGTTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 6301
QY 1441 TGTAGCAGAGTCTCTGTTGGGTCACACCGCCCTCAGCACAGCACTTTGAGTTTGGTA 1500
DB 6302 TGTAGTATAGTCTGTTTGGGGTTATACGTCGGTTTATAGTATAGTATTTTGGAGTTTGGTA 6361
QY 1501 CTACGTTATCCACATTTTACATGACAGAAATGAGGATGAGGATGAGGATGAGGATGAGG 1560
DB 6362 TTACGTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 6421
QY 1561 CAAATTTTATTTCAATGCTACCTGCGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
DB 6422 TAAATTTTATTTTAAATGTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 6481
QY 1621 TATGATTTTAAACATCAGCTGCAATGAGGTTGAAATTAATTAATTAATTAATTAATTAATTA 1680
DB 6482 TATGATTTTAAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 6541
QY 1681 AATATTTCAATGTTTCAAGTGTAAATGAGTCCAGCCCATGTTGTCACCTGTTCAAGCCC 1740
DB 6542 AATATTTTATTTTATAGTGTAAATGAGTTTATTTATTTATTTATTTATTTATTTATTTATTT 6601

QY 1741 CAAGGAGAGACAGGAAACAGTCTTTACCTTTGATATTTTCATCTAGTGGAGA 1800
 DB 6602 TAAGGAGAGAGTAGGAAATAGTTTTATTTTGTATATTTTGTATTTTAGTGGAGA 6661
 QY 1801 GATGACAAATAGCAATAGCAGAAAGATATACACATCAGGAAATCATGGGTGTGTGA 1860
 DB 6662 GATGATATATAGTAATAGTAGAAAGATATATATATATAGGAATATGGGTGTGTGA 6721
 QY 1861 GAAGCAGAGAAGTCAGGCAAGTCACTCTGGGCTGACACTTTGACGAGACATGAAGA 1920
 DB 6722 GAAGTAGAGAAGTAGGGTAAAGTATTTTGGGCTGATATTTGAGTAGAGATATGAAGA 6781
 QY 1921 AATAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTGGCAAG 1980
 DB 6782 AATAGAAATGATTTGATTTGGGAGTAGTATTTTATAGGTAATCAGTGGGTTCGTAAAG 6841
 QY 1981 TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
 DB 6842 TTGGATTTAAAGACGGGTTTTTATAGTATTTATGTGTGTGTGGGGGGGGGGGG 6901
 QY 2041 CGCGTGGGGTGGAAAGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT 2100
 DB 6902 CGCGTGGGGTGGAAAGGGGATTTATTTGTATGTAGGATGTTTAGTAGTATTTTGT 6961
 QY 2101 CCTCCCTACTACTAGTGTCTAGGAGCAGTCTCCCGAGTCTTACAAACCAAAATGCTCT 2160
 DB 6962 TTTTATTTATTTATAGGTATAGGAGTATTTTATAGTATTTTATTAATAATGTTTTT 7021
 QY 2161 AAATTTTGGCCATGTCTACTAGTAGACAAATCTCTGGTTAAGAAAGCTCGGGTTCAAAA 2220
 DB 7022 AAATTTTGTATATGTATTTATAGTAGATAAATTTTGTGTAGAAAGTTCGGGTGA 7081
 QY 2221 AATAAACAGTAGTGTCTGGGAGTAGAGCCCAAGAGTAGTAAATGGGCTCAGAAAGAGA 2280
 DB 7082 AATAAAATAGTAGTGTGGGAGTAGAGGTTAAGAAAGTAGTAAATGGGTTAAGAGAGA 7141
 QY 2281 GCCAAACAAAGGTTGTGCAGGCGCTGTAGGCTGTGTGTGTGAATCTTAGCCAAAGAGTA 2340
 DB 7142 GTTATAAATAGGTTGTGTAGGCGTTGTAGGTTGTGTGTGAATTTTAGTTAAGGAGTA 7201
 QY 2341 ACAGTGTATCTGTACAGGCTTTTAAAGANTCTCTGGCTGTATGTGGAAAGCAGAAATG 2400
 DB 7202 ATAGTGTATTTGTATAGGTTTTTAAAGANTCTTTTGGTTGTATGTGGAAAGTAGAATG 7261
 QY 2401 AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGGAGCTGTATACAGTCCAGGCAAG 2460
 DB 7262 AAGGAGTAAATAGTAAAGTAGGAGTTTAGTTAGGAAGTTGTATATAGTTTAGGTAAG 7321
 QY 2461 AGGTAGTGGAGTGGGCTGGGTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCTGAA 2520
 DB 7322 AGGTAGTGGAGTGGGTTGGGTGGGAAATAGAAAGGGAGTGATAAATTTATTTTGA 7381
 QY 2521 TATATTTCTGAAGAAAGTGTCTCAAGATTTCTATTTGTGTGAGAAAGAGAAATTTGG 2580
 DB 7382 TATATTTTGAAGAAAGTGTCTCAAGATTTTATTTGTGTGAGAAAGAGAAATTTGG 7441
 QY 2581 CTGGGTGTAGTACTCATCCAGGAGGAGCCAGGAGAGCAGATTCCTGAGCTCAGGA 2640
 DB 7442 TTGGGTGTAGTATTTATGTTAAGGAGGAGTTAAGGAGAGTAGATTTTGTAGTTTAGA 7501
 QY 2641 GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTTCTTACAAAATATACAAAATTA 2700
 DB 7502 GTTAAAGATTTAGTTTGGGTAAATATAGTAAATTTTTTTTTTATATAAAAATATANA 7561
 QY 2701 GCTGGGTGTGGTGGCATGCCTGTGATCTAGTACTCGGAGGCTGAGGTGGAGGTA 2760
 DB 7562 GTTGGGTGTGGTGGTATGTATTTGTGATTTTATTTAGTTATTCGGAGGTTGAGGTGG 7621
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 DB 8581 TTTTATTTATATATAGTTTAAAGTTTGTGTTTGTGTTTGTAGG 8622

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 09:06:57 ; Search time 15746.3 Seconds
(without alignments)

12086.738 Million cell updates/sec

Title: US-09-497-957-1_COPY_1_5000

Perfect score: 5000

Sequence: 1 TCTAAGGTTGAGATAAAATT.....GCTAATTGGAAGCTGAGGC 5000

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	612.8	12.3	691	4	BG926549 HNC42-1-G
C 2	589	11.8	648	9	AG116246 Pan trogl
C 3	464.2	9.3	531	8	AQ703007 HS_5443_B
C 4	420.8	8.4	442	2	AW449998 UI-H-BI3-
C 5	412.6	8.3	533	8	AQ790990 HS_2239_B
C 6	408.4	8.2	443	8	AQ111002 CIT-RSP-2
C 7	313.4	6.3	326	8	AQ056874 CIT-RSP-2
C 8	298	6.0	603	7	CN264281 170005313
C 9	293	5.9	420	8	AQ296898 HS_3005_B
C 10	281.6	5.6	3713	3	BC041839 Homo sapi
C 11	277.4	5.5	6146	8	AQ839831 260L13-C4
C 12	268.8	5.4	793	4	BM551225 AGENCOURT
C 13	267.2	5.3	5940	3	CR627133 Homo sapi
C 14	266.2	5.3	972	5	BQ712091 AGENCOURT
C 15	266	5.3	570	2	BE272926 601171213
C 16	265	5.3	819	4	BG747345 602704818
C 17	264	5.3	544	4	BM751283 K-EST0027
C 18	264	5.3	560	1	AU279987 AU279987
C 19	264	5.3	3288	3	HSMB02613
C 20	262.4	5.2	535	6	CB162561 K-EST0223
C 21	259.4	5.2	6056	3	CR627178 Homo sapi
C 22	258.4	5.2	2009	3	HSMB02716
C 23	258.2	5.2	714	6	CD366358 UI-H-FT1-
C 24	256	5.1	4975	8	AQ839811 260L13-C4

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C 27	252.8	5.1	4207	3	BC034315	BC034315 Homo sapi
C 28	251.8	5.0	761	5	BQ707017	BQ707017 AGENCOURT
C 29	250.8	5.0	1723	3	BC039095	BC039095 Homo sapi
C 30	247.6	5.0	741	7	CR748096	CR748096 CR748096
C 31	245.8	4.9	6789	3	HSMB07629	BX647483 Homo sapi
C 32	245.2	4.9	1374	3	BC017002	BC017002 Homo sapi
C 33	242.4	4.8	4750	3	HSMB04795	AL833482 Homo sapi
C 34	242.2	4.8	2455	3	AF461900	AF461900 Homo sapi
C 35	242	4.8	724	6	CA427092	CA427092 UI-H-DF0-
C 36	240	4.8	388	2	AW069227	AW069227 cr41h09.x
C 37	239	4.8	2531	3	BC020559	BC020559 Homo sapi
C 38	238.6	4.8	731	7	CN307840	CN307840 170004182
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C 40	238	4.8	3863	3	BC035034	BC035034 Homo sapi
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C 42	237.2	4.7	1300	8	AF057104	AF057104
C 43	237	4.7	735	7	CF146929	CF146929 UI-HF-CB0
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C 45	236.6	4.7	647	4	BM559057	BM559057 AGENCOURT

ALIGNMENTS

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DEFINITION HNC42-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG926549
VERSION BG926549.1 GI:14321072
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 691)
AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.
TITLE Identification and initial characterization of 5000 expressed sequence tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7
Location/Qualifiers
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1. .691
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
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/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN

Query Match 12.3%; Score 612.8; DB 4; Length 691;
Best Local Similarity 98.9%; Pred. NO. 1e-83;
Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1397 TACAGCTGCTTCTAACTTAGTTAGTACAGTATTTGCCCTGTAGTCACAGTGTCT 1456

Db 691 TACAGTGTCTTAATCTTAGTTGACAGTGAATTTGCCCTGTAGTGTAGCAGAGTGTCT 632
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Db 511 TACACTGGCTTTGGTGGCAGAGCTCATGCTCTCACTTCATAGCTATGATCTTCAACAT 452
QY 1637 CACACTGCATTAGAGGTTGAATAATAAATTTTCATGTTGAGCAGAAATATTCATGTTTA 1696
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QY 1697 CAAGTGTAAATGAGTCCCGCCATGTTGCACTGTTCAAGCCCAAGCGGAGAGCAGG 1756
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Db 271 TGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGAGAAGCAGAGAACTCAG 212
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Db 211 GCGAAGTCACTCTGGGGCTGACACTTGAGCAGAGACATGAAGGAAATAAGATGATTTG 152
QY 1937 ACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTCGCAGTTGGATTAAAGCGG 1996
Db 151 ACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTCGCAGTTGGATTAAAGCGG 92
QY 1997 GTTTTCTCAGCACTACTCATGTGT 2020
Db 91 GTTTTCTCAGCGGACGCGTGGGT 68

RESULT 2
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Pan troglodytes DNA, clone: PTB-123L15.R, genomic survey sequence.
AG116246
AG116246.1 GI:16736765
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 648)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpses@gsc.riken.go.jp; URL:http://hgp.gsc.riken.go.jp/)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS

Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
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Best Local Similarity 99.2%; Pred. No. 4.4e-80;
Matches 592; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 288 TAATCTGGTTTCTGATGTTATTTCAAGTACTACAGCTCTCTTAATCTTAGTTGACGT 229
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QY 1486 CTTTTCAGTTTGGTACTACGTGTATTCACATTTTACATGACAGCAATGAGCATGGCA 1545
Db 168 CTTTTCAGTTTGGTACTACGTGTATTCACATTTTACATGACAGCAATGAGCATGGCA 109
QY 1546 CGGCTGCTCTCTCGCAAAATTTATTCATGTTGATGTTGCTGGTGGCAGAGCTC 1602
Db 108 CGGCTGCTCTCTCGCAAAATTTATTCATGTTGATGTTGCTGGTGGCAGAGCTC 52
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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genomic clone Plate=1019 Col=17 Row=N, genomic survey sequence.
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AQ703007.1 GI:5412433
GSS.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 531)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas G, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1019 row: N column: 17
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Best Local Similarity 96.5%; Pred. No. 5.2e-61;
Matches 472; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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DB 222 TTCTGCCCTTACTCTAGTGGCAGAGGTGGAGGGTTTCAGGCACGGATCCCTGGTT 281
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DB 282 GGAGTTTCAGAGGTGGCTGAGGCTGTGTGCTCTTCCAAATCTTGGGAAGGACTTTCTCA 341
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DB 342 ATCTAGAGTCTTACTTAAATGAGATGTATGACAGCCACCAAGTCATGGGTTAA 401
QY 4708 TTCTTTTCCATGATATGGCTCAAGGAAGTGTCTATGGCCCTTCTTTTATTTA 4767
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QY 4768 ACCAATAATCTTTGTATATTTATACCTGTTAAAAATTCAGAAATGTCAAGCCGGGCAC 4827
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QY 4828 GTTGGCTCA 4836
DB 522 GTTGGCTCA 530
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-1@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: www-bio.lnl.gov/bbrp/image/image.html
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/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub5 is a subtracted library derived from NCI CGAP Sub4. The NCI CGAP Sub5 library had 3 million recombinants. A single-stranded DNA preparation of NCI CGAP Sub4 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Col0 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE CloneIDs 2708616-2710535) and NCI CGAP Sub2 (IMAGE CloneIDs 2710536-2712455) (10% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE CloneIDs 2723592-2728969) (70% of the

driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISSUE=colon
TAG_LIB=NCI CGAP_Col0
TAG_SEQ=AAACG"

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ORIGIN
Query Match      8.4%; Score 420.8; DB 2; Length 442;
Best Local Similarity 99.5%; Pred. No. 2.3e-54;
Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 325 GAGATTAAACGGGAGCGTGGCGCAGAGCTGGGGAATGGCCCGCAGCAGCGCCGGG 384
Db 440 GGGATTAAACGGGAGCGTGGCGCAGAGCTGGGGAATGGCCCGCAGCAGCGCCGGG 381
QY 385 CTTCTCCTCTGATGCTTTTCAGACCGCGGTCTCGAGGGGCGCTTGTGGTGAGTCC 444
Db 380 CTTCTCCTCTGATGCTTTTCAGACCGCGGTCTCGAGGGGCGCTTGTGGTGAGTCC 321
QY 445 GAGGGCTGGCGGGAACCTAGGGCGCGCGGGGTGAAAAATCGAAACCTAGCTTTTCT 504
Db 320 GAGGGCTGGCGGGAACCTAGGGCGCGCGGGGTGAAAAATCGAAACCTAGCTTTTCT 261
QY 505 TTGCGCTTGGGAGTTGTAACTTTTGAGACCTGCTCAACCTATCCGCAAGCCCTCT 564
Db 260 TTGCGCTTGGGAGTTGTAACTTTTGAGACCTGCTCAACCTATCCGCAAGCCCTCT 201
QY 565 CCTACTTTCTGGTCCAGACCCCGTGAGGAGTGCTTACCCTGAACTGCAGATAGGG 624
Db 200 CCTACTTTCTGGTCCAGACCCCGTGAGGAGTGCTTACCCTGAACTGCAGATAGGG 141
QY 625 TCCTCGCCCCAGGACCTGCCCTCCCGCGTGTCCCGGCTCTCGGAGTGACTTTTG 684
Db 140 TCCTCGCCCCAGGACCTGCCCTCCCGCGTGTCCCGGCTCTCGGAGTGACTTTTG 81
QY 685 GAACCGCCACTCCCTTCCCGCACTAGATGCTTTTAAATAAATCTCGTAGTTCCTAC 744
Db 80 GAACCGCCACTCCCTTCCCGCACTAGATGCTTTTAAATAAATCTCGTAGTTCCTAC 21
QY 745 TTGA 748
Db 20 TTGA 17
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RESULT 5
LOCUS
DEFINITION
  A0790990/c
  HS 2239_B1_D04_MR CIT Approved Human Genomic Sperm Library D Homo
  sapiens genomic clone Plate=2239 Col=7 Row=H, genomic survey
  sequence.
ACCESSION
  A0790990
  A0790990.1 GI:5698614
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
  Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
  Hood, L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL
  MEDLINE
  PUBMED
  1049764
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
```

Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2239 row: H column: 7
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 533.

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      E-Coli DH10B"
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ORIGIN

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Query Match      8.3%; Score 412.6; DB 8; Length 533;
Best Local Similarity 91.6%; Pred. No. 3.9e-53;
Matches 447; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

QY 2685 AAAAAACAAAAAATTAGCTGGGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGGAG 2744
Db 533 AAAAAACATAAATATAGTGTGTGGTGGCATGCACTTGTGATCCTAGCTACTCGGAAG 474
QY 2745 GCTGAGGTGGAGGGTATTGCTTGAGCCCAAGGTTGAGGCTGCAGTGAGCCATGCTGT 2804
Db 473 CTGAGGTGGAGGGTATTGCTTGAGCCCAAGGTTGAGCTGCAAGTGAGCAATGACTGT 414
QY 2805 GCCACTGTACTTCAGCTAGGTGACAGACAGACCCCTGTCTCCCTGACCCCTGAAAA 2864
Db 413 GCCACTGTATTCAAGCTAGGTGACAGACAGACCCCTGTCTCCCTGACCCCTGAAAA 354
QY 2865 ACAGAGAGCTTAAAGTTGACTTTGTTCTTTTAAATTTTAAATTTTAAATTTTAAAT 2924
Db 353 ACAGAGAGCTTAAAGTTGACTTTGTTCTTTTAAATTTTAAATTTTAAATTTTAAAT 294
QY 2925 TAAATGGCAATGCCATTTCTGAGATGGTGAAGCGAGAGAAAGACAGATTTGGGGTAAAT 2984
Db 293 TAAATGGCAATGCCATTTCTGAGATGGTGAAGCGAGAGAAAGACAGATTTGGGGTAAAT 234
QY 2985 CAAGATCTGCATTTGGGACATGTTAAGTTTGAGATTCAGTCAGCTTCCAGTGGTGA 3044
Db 233 CAAGATCTGCATTTTGGACATGTTAAGTTTGAGATTCAGTCAGCTTCCAGTGGTGA 175
QY 3045 GGCACATAGGAGCTTTCAGTGTAAAGATTCAGGACCAAGGCTGGGACGGTGCTCACIT 3104
Db 174 GGCACATAGGAGCTTTCAGTGTAAAGATTCAGGACCAAGGCTGGGACGGTGCTCACIT 115
QY 3105 CTGTAAATCCAGCAGCTTTGGTGGCTGAGGAGGTAGATCAATTTGAGGTGAGGTTTGG 3164
Db 114 CTGTAAATCCAGCAGCTTAAAGGAGCTGAGGAGGTAGATCAATTTGAGGTGAGGTTTGG 55
QY 3165 ACAGCTT 3172
Db 54 ACATGCTT 47
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RESULT 6

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LOCUS
DEFINITION
  A0111002/c
  CIT-HSP-2370L14.TR CIT-HSP Homo sapiens genomic clone 2370L14,
  genomic survey sequence.
ACCESSION
  A0111002
  A0111002.1 GI:3487692
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE 1 (bases 1 to 443)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
 Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other GSSs: CIT-HSP-2370L14.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

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 /clone_lib="CIT-HSP"
 /notes="Vector: pBelobAC11; Site_1: HindIII; Site_2:
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 Best Local Similarity 99.5%; Pred. No. 1.8e-52;
 Matches 420; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Db 2752 TGGAGGGTATTGCTTGAGCCCGAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTG 2811
 |||||
 443 TGAAGGGTATTGCTTGAGCCCGAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTG 384
 |||||
 2812 TACTTCAGCTAGTGCAGAGCAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAG 2871
 |||||
 383 TACTTCAGCTAGTGCAGAGCAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAG 324
 |||||
 2872 AGTTAAAGTTGACTTGTCTTTATTTTAAATTTTATTGGCTGAGCAGTCGGGTAAATTGG 2931
 |||||
 323 AGTTAAAGTTGACTTGTCTTTATTTTAAATTTTATTGGCTGAGCAGTCGGGTAAATTGG 264
 |||||
 2932 CAATGCCATTTCTGAGATGGTGAAGGCAGAGGAAGCAGATTTGGGGTAAATCAAGGAT 2991
 |||||
 263 CAATGCCATTTCTGAGATGGTGAAGGCAGAGGAAGCAGATTTGGGGTAAATCAAGGAT 204
 |||||
 2992 CTCGATTTGGGACATGTTAAGTTTGAATTCAGATCCAGGCTTCAAGTGTGTGAGGCCACA 3051
 |||||
 203 CTCGATTTT-GGACATGTTAAGTTTGAATTCAGATCCAGGCTTCAAGTGTGTGAGGCCACA 145
 |||||
 3052 TAGGCAGTTCAGTGAAGATTCAGGACCAAGCTGGGCACGGTGGCTCACTTCTGTAT 3111
 |||||
 144 TAGGCAGTTCAGTGAAGATTCAGGACCAAGCTGGGCACGGTGGCTCACTTCTGTAT 85
 |||||
 3112 CCCAGCACTTTGGTGGCTGAGGCGAGGTAGATCATTTTGAAGTTCAGGATTTGAGACAAGCT 3171
 |||||
 84 CCCAGCACTTTGGTGGCTGAGGCGAGGTAGATCATTTTGAAGTTCAGGATTTGAGACAAGCT 25
 |||||
 3172 TG 3173
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 24 TG 23

RESULT 7
 AQ056874/c
 LOCUS 326 bp DNA linear GSS 30-JUL-1998

DEFINITION CIT-HSP-2339H7.TR CIT-HSP Homo sapiens genomic clone 2339H7,
 genomic survey sequence.
 ACCESSION AQ056874
 VERSION AQ056874.1 GI:3353480
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 326)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M. and Venter,J.C.
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other GSSs: CIT-HSP-2339H7.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
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 HindIII"

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 Best Local Similarity 99.4%; Pred. No. 6.3e-38;
 Matches 325; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 2839 CCTGTCTCCCTGACCCCTGAAAGAGAGAGTAAAGTTGACCTTGTCTTTATTT 2898
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 326 CCTGTCTCCCTGACCCCTGAAAGAGAGAGTAAAGTTGACATTTGTTCTTTATTT 267
 |||||
 2899 TAATTTTATTTGGCTCAGCAGTCGGGTAAATGGCAATGCCATTTCTGAGATGGTGAAGGC 2958
 |||||
 266 TAATTTTATTTGGCTCAGCAGTCGGGTAAATGGCAATGCCATTTCTGAGATGGTGAAGGC 207
 |||||
 2959 AGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTTGGGACATGTTAAGTTTGAG 3018
 |||||
 206 AGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTT-GGACATGTTAAGTTTGAG 148
 |||||
 3019 ATTCAGTCAGGCTTCAAGTGTGTGAGGCCACATAGCAGTTCAAGTGAAGAATTCAGGA 3078
 |||||
 147 ATTCAGTCAGGCTTCAAGTGTGTGAGGCCACATAGCAGTTCAAGTGAAGAATTCAGGA 88
 |||||
 3079 CCAAGCTGGGACGGTGGCTCACTTCTGTAATCCAGCACTTTGGTGGCTGAGGCAAGGT 3138
 |||||
 87 CCAAGCTGGGACGGTGGCTCACTTCTGTAATCCAGCACTTTGGTGGCTGAGGCAAGGT 28
 |||||
 3139 AGATCATTTTTCAGGTCAGGAGTTTGAGA 3165
 |||||
 27 AGATCATTTTTCAGGTCAGGAGTTTGAGA 1

RESULT 8
 CN264281

LOCUS CN264281 603 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000531346032 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN264281
VERSION CN264281.1 GI:47280695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 603)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Brandenberger R., Wei, H., Zhang S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J and Stanton, L. W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 603 Std Error: 0.00.
Location/Qualifiers
1. .603
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derived from H1, H7 and H9 cells"
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from embryoid body outgrowths derived from HES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
ORIGIN
Query Match 6.0%; Score 298; DB 7; Length 603;
Best Local Similarity 71.2%; Pred. No. 1.2e-35;
Matches 517; Conservative 0; Mismatches 0; Indels 209; Gaps 1;
QY 3762 GTTCACACTCTGCACTACCTCTTCATGGTGGCTCAGACAGGACCTTGGTCTTCT 3821
Db GTTCACACTCTGCACTACCTCTTCATGGTGGCTCAGACAGGACCTTGGTCTTCT 146
QY 3822 TGTTTGAAGCTTTGGGCTAGCTGGATGACAGCTGTTCTGTTCTATGATCATGAGATC 3881
Db TGTTCGAAGCTTTGGGCTAGCTGGATGACAGCTGTTCTGTTCTATGATCATGAGATC 206
QY 3882 GCGGTGTGGAGCCCGAATCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941
Db GCGGTGTGGAGCCCGAATCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 266
QY 3942 AGCTGAGTCAGATCTGAAGGGTGGATCACATGTTCTACTGTTGACTTCTGACATATTA 4001
Db AGCTGAGTCAGATCTGAAGGGTGGATCACATGTTCTACTGTTGACTTCTGACATATTA 326
QY 4002 TGGAAATACACACACAGCAAGGGTATGTGGAGAGGGGCGCTCACCTTCTGAGGTGT 4061
Db TGGAAATACACACACAGCAAGGGTATGTGGAGAGGGGCGCTCACCTTCTGAGGTGT 349
QY 4062 CAGAGCTTTTTCATCTTTTTCATGTCATCTTGAAGGAAACAGCTGGAAGTCTGAGCTTGTG 4121
Db CAGAGCTTTTTCATCTTTTTCATGTCATCTTGAAGGAAACAGCTGGAAGTCTGAGCTTGTG 349
QY 4122 GGAGCAGGGAAGAGGGAAGGAATTTGCTTCTCAGATCATTTGGTCTTGGGATGGTGG 4181
Db GGAGCAGGGAAGAGGGAAGGAATTTGCTTCTCAGATCATTTGGTCTTGGGATGGTGG 349
QY 4182 AAATAGGACCTATTCTTTGTTGAGTTTAAACAAGGCTGGGATTTTTCAGAGTCCCA 4241
Db AAATAGGACCTATTCTTTGTTGAGTTTAAACAAGGCTGGGATTTTTCAGAGTCCCA 357

QY 4242 CACCTCGCAGGTTCATCTCTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTG 4301
Db CACCTCGCAGGTTCATCTCTGGGCTGTGAATGCAAGAACAACAGTACCGAGGGCTACTG 417
QY 4302 GAAGTACGGGTATGATGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAG 4361
Db GAAGTACGGGTATGATGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAG 477
QY 4362 ACAGCAGAACCCAGGGCTGCGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTGGGC 4421
Db ACAGCAGAACCCAGGGCTGCGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTGGGC 537
QY 4422 CAGGAGAACAGGGCTACCTCGAGAGGAGTGCCTCGACAGTGCAGCAGTTGCTGGA 4481
Db CAGGAGAACAGGGCTACCTCGAGAGGAGTGCCTCGACAGTGCAGCAGTTGCTGGA 597
QY 4482 GCTGGG 4487
Db GCTGGG 603
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DEFINITION sapiens genomic clone Plate=3005 Col=17 Row=F, genomic survey
sequence.
ACCESSION AQ296898
VERSION AQ296898.1 GI:4014077
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 420)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3005 row: F column: 17
Class: BAC ends
High quality sequence stop: 420.
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Best Local Similarity 89.2%; Pred. No. 7.6e-35;
Matches 357; Conservative 0; Mismatches 37; Indels 6; Gaps 4;
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Db 1 .ACGACCAAGCTGGGCAAGGCTGCTCACTTATGTAATCCACGACATTTGGTGGCTGAGGC 60

Qy 3135 AGGTAGATCATTTGAGGTCAGAGTTTGAGACAAGCTTGGCCAAACATGCTGAAACCCCAT 3194

Db 61 ANGTAGATCATTTGAGGTCAGAGTTTGAGACAAGCTTGGCCAAACATGCTGAAACCCCAT 120

Qy 3195 GTCTACTAAATAACAAAAATTAGCTGGTGTGGTGGCGCACGCTATAGTCCAGGTTT 3254

Db 121 GTCTACTAAATAACAAAAATTAGCTGGTGTGGTGGCGCACGCTATAGTCCAGGTTT 180

Qy 3255 TCAGGAGCTTAGTGTAGAGATCCCTTGAACCCAGAGGTGCAGTTGCACTGAGCTGA 3314

Db 181 TCAAGAGCTTAGTGTAGAGATCCCTTGAACCCAGAGGTGCAGTTGCACTGAGCTGA 240

Qy 3315 GATTGTGCACTGCACTCCAGCTGGGTGATAGTGTGAGACTCTGTCTCAAA--AAAAA 3372

Db 241 GATTGTGCACTGCACTCCAGCTGGGTGATAGTGTGAGACTCTGTCTCAAGNCCATNAC 300

Qy 3373 AAAAAAATAAAAAAATAAAAACTGAAGGAATTATTCCTCAGGATTTGGGTCTTAATTTGCC 3432

Db 301 TNCATACNCTCTTAAAACTGCAGGAATTATT-CTCAGGATTTGGGTCTAA--TGCC 357

Qy 3433 TGACACCAACTCTGATTTCAATACCATGCTAGACAC 3472

Db 358 CTGACACCAACTGCTGAG-TCAACTACCATGTTAACACAC 396

RESULT 10

BC041839/c
LOCUS BC041839 3713 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, similar to expressed sequence AW111961, clone IMAGE:5268751, mRNA.

ACCESSION BC041839
VERSION BC041839.1 GI:27693117
KEYWORDS HTC.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3713)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (23-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Tohiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES
source

RESULT 11
AQ839831
LOCUS AQ839831
DEFINITION 260L13-C47 CITB Homo sapiens genomic clone 260L13, genomic survey sequence.
ACCESSION AQ839831
VERSION AQ839831.1 GI:6652463
KEYWORDS GSS.
SOURCE Homo sapiens (human)

/note="Vector: pBluescript"

Query Match 5.6%; Score 281.6; DB 3; Length 3713;
Best Local Similarity 65.6%; Pred. No. 2.2e-33;
Matches 542; Conservative 0; Mismatches 234; Indels 50; Gaps 7;

Qy 2578 TGGCTGGGTGTAGTAGTCTATGCGCAAGGAGGAGGCCAAGGAGAGACAGATTCTCGAGCTCA 2637

Db 2275 TGGCTCATGCTGTATGTCACGCACTTTGGGAGGCCGAGGCGAGAG-TACGAGGTCA 2217

Qy 2638 GGAGTTCAAGACCAAGCTGGGCAACACAGCAAAAAACCCCTTCTCTACAAAAAATACAAAA 2697

Db 2216 AGAGATCAAGACCACTCTGGCCAACTGGTGAACCCCATCTCTACTTAAATAACAAAA 2157

Qy 2698 TTAGCTGGGTGTGGTGGCATGCACCTGTGATCTTAGTACTTCGGGAGGCTGAGGTGGAGG 2757

Db 2156 TTAGCTGGGTGTGGTGGCATGCACCTGTGATCTTAGTACTTCAGGAGGCTGAGGCGAG-GA 2098

Qy 2758 GTATTGTCTTGAGCCCAAGAGTTTGAGGCTGCAGTGAGCCATGACTGTGCGCACTGTACTTC 2817

Db 2097 GAATCACTTGAACTGGAGGTGGAGTTTGCAATGAGCCAAAGATGTCCCACTGCATTTCC 2038

Qy 2818 AGCTTAGGTGACAGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAA 2877

Db 2037 AGCTGGGCGACAGAGCAAGACTCCATCTCAAAACAACAACAACAACAACAACAACAACA 1978

Qy 2878 AGTTGACTTGTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2937

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

CONSTRM

TITLE

JOURNAL

COMMENT

CR627133

Homo sapiens mRNA; cDNA DKFp686J154 (from clone DKFp686J154).

CR627133.1

GI:50949747

HTC

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5940)

Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

The German cDNA Consortium

Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Dueseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFp686J154) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFp686J154

Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

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location/Qualifiers

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Best Local Similarity 64.7%; Pred. No. 3e-31;

Matches 489; Conservative 0; Mismatches 238; Indels 29; Gaps 5;

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Db 4788 TACAAAAATTAGCTAGTGTGGTGTGGCTGTAGCTCTTGTACTCGGAGGCTGA 4729

Qy 2750 GTTGGAGGTTATTTGTTGAGCCAGGAAGTTGAGGCTGAGGCTGAGCCATGACTGTGCCAC 2809

Db 4728 GGTG--GGGATCGATTGAGCCGGGAAGTTGAGGCTGAGTGCAGCAAGATTGTGCGAT 4671

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Db 4670 TGCACCTCCAGCCCTGGGCAACACAGCAAAACCCCTGTCAACATGAAAAAGACAAC 4611

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Qy 2930 GGCAATGCCATTTCTGAGATGTGAAAGGCGAGAGGAAGAGCAGTTTGGGTTAAATCAAGG 2989

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Qy 3169 GCTTGGCCCAACATGTGTGAACCCCATGTCTACTTAAATAATAC--AAAAATTAGCTGTGTG 3227

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VERSION
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 972)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Query Match 5.3%; Score 266.2; DB 5; Length 972;
Best Local Similarity 63.4%; Pred. No. 7.3e-31;
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QY 2628 CTTGAGCTCAGGAGTTCAAGACCAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAA 2687
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ACCESSION
BE272926
VERSION
BE272926.1 GI:9147279
KEYWORDS
EST.
Homo sapiens (human)
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 570)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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/note="Organ: kidney; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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FEATURES
source

ORIGIN

Query Match 5.3%; Score 266; DB 2; Length 570;
Best Local Similarity 91.8%; Pred. No. 9.2e-31;
Matches 292; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

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; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; CLASSIFICATION: 514
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; LOCATION: 6040..6153, 7107..7147)
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; OTHER INFORMATION: normal or wild-type (unaffected) genomic
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; NAME/KEY: -
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; OTHER INFORMATION: /note= "start and stop positions for
; OTHER INFORMATION: normal or wild-type (unaffected) genomic
; OTHER INFORMATION: sequence surrounding variant for 24d2(C)
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Qy 661 CCGGCTCTCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGATGCTTT 720
Db 661 CCGGCTCTCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGATGCTTT 720

Qy 721 TAAATAAATCTCGTAGTTCCTCACTGAGCTGAGCTAAGCTGAGGCTCTTGAACCTGG 780
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Qy 781 AACTCGGGTTTATTTTCCAATGTGAGCTGTGAGTGTTCCTTCCCCAGTCACTCCAAACAGG 840
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Qy 1141 CTAGGCTTTATGATTTGCAATGTGTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200
Db 1141 CTAGGCTTTATGATTTGCAATGTGTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200

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; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; OTHER INFORMATION:
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LOCATION: replace(5834, "a")
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US-08-834-497A-3

Query Match 100.0%; Score 5000; DB 3; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
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US-09-503-444A-1
; Sequence 1, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchinashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
; LOCATION: 6040..6153, 7107..7147)
; OTHER INFORMATION: /product= "Hereditary Hemochromatosis"
; OTHER INFORMATION:
; OTHER INFORMATION: /note= "No. 6228594mal or wild-type (unaffected)"
; OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene
; OTHER INFORMATION: allele"
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RESULT 6
US-09-503-444A-3
; Sequence 3, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/630,912
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; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/POCKET NUMBER: 8907-0088-999
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
; LOCATION: 6040..6153, 7107..7147)
; OTHER INFORMATION: /product= "Hereditary Hemochromatosis"
; OTHER INFORMATION: mutation"
; OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)"
; OTHER INFORMATION: gene 24d1 allele"
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Db	194884	CTGGGTGTAGTACTCATGCTCAAGAGAGGAGGCCAAGAGAGACAGATTTCTGTAGCTCAGGA	194943	QY	3721	CTCTTACTACACATGGTTAAGCCCTGTGTCTCTGTCTCCAGGTTTCACTCTCTGCACTA	3780
QY	2641	GTTCAAGACAGCCTCGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700	Db	196024	CTCTTACTACACATGGTTAAGCCCTGTGTCTCTGTCTCCAGGTTTCACTCTCTGCACTA	196083
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Db 196924 TCCAAATCTGGGAAGGACITTTCTCAATCCTAGAGTCTCTACCTTATAATTGAGATGTA 196983
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RESULT 8
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; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolfe, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
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; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US-08-724-394A-21
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1141	CTAGGCTTTATGATTTGCAATGTGTCTGTGTAAATTAAGAGCCCTCTCTACAAAGTACTGA	1200		Db	194524	AATAAACAAGTAGTGTCTGGGAGTAGAGCCCAAGAGTAGGTAAATGGGGTCTAGAGAGGA	194583
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QY	1441	TGTAGCACAGTGTCTGTGGGTCAACGCGCGGCTCAGCACAGCACTTTTGAAGTTTGGTA	1500		Db	194824	TATATTTCTGAAGAAATTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATTTGG	194883
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/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/724,394A
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitts, Renee A.
/ REGISTRATION NUMBER: 35,136
/ REFERENCE/DOCKET NUMBER: 017957-000100
/ TELEPHONE: 415-576-0200
/ TELEFAX: 415-576-0300
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 246240 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
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/ MOLECULE TYPE: cDNA
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/ NAME/KEY: misc feature
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/
US-08-724-394A-22

Query Match 100.0%; Score 5000; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy	1921	AATAAGAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTCGCAAG	1980
Db	194224	AATAAGAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTCGCAAG	194283
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Qy	2881	TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAATTTGGCAATGCCAT	2940
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Db	195244	TTCTGAGATGTAAGCAGAGGAAGCAGTGTGGGGTAAATCAAGGATCTGCATTTG	195303
Qy	3001	GGACATGTTAAGTTTTCAGATTCAGGCTTCCAAAGTGTGAGGCCACATAGGCAGTT	3060
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 ; Sequence 5, Application US/08652265
 ; Patent No. 6025130
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Winston J.
 ; APPLICANT: Drayna, Dennis T.
 ; APPLICANT: Feder, John N.
 ; APPLICANT: Gnirke, Andreas
 ; APPLICANT: Ruddy, David
 ; APPLICANT: Tsuchihashi, Zenta
 ; APPLICANT: Wolff, Roger K.
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,265
 ; FILING DATE: 23-MAY-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 17957-000500
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10825 base pairs
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 ; STRANDEDNESS: single
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; OTHER INFORMATION: /label= 24d2
US-08-652-265-5

Query Match 100.0%; Score 4998.4; DB 3; Length 10825;
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QY 61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCCAATCAACAACCCCT 120
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RESULT 11

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US-08-652-265-7
; Sequence 7, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Teuchihaishi, Zenta

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; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
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OTHER INFORMATION: /label= 24d1
US-08-652-265-7

Query Match 100.0%; Score 4998.4; DB 3; Length 10825;
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RESULT 12

US-08-834-497A-5
; Sequence 5, Application US/08834497A
; Patent No. 6140305

GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Teuchihaishi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 10825 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

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LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis

OTHER INFORMATION:

OTHER INFORMATION: mutation"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)

OTHER INFORMATION: gene 24d2 allele"

NAME/KEY:

LOCATION: 140..7319

OTHER INFORMATION: /note= "start and stop positions for

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FEATURE:

NAME/KEY:

LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for

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FEATURE:

NAME/KEY:

LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"

FEATURE:

NAME/KEY: allele

LOCATION: replace(3872, "g")

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis

OTHER INFORMATION:

OTHER INFORMATION: /label= 24d2

US-08-834-497A-5

Query Match

Best Local Similarity

Matches 4999; Conservative

100.0%; Score 4998.4; DB 3; Length 10825;

100.0%; Pred. No. 0;

Mismatches 0; Indels 1; Gaps 0;

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DB 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTTTGAATTTTGAATAATCATTAATATTTA 60
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DB 61 AATATCTAAAGTTTCAGATCAGAAACATTTGCGAAGCTACTTTCCCAATCAACAACACCCCT 120
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DB 121 TCAGGATTTAAACCAAGGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT 180
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DB 301 TTTCCCGCCCCCAAGGAAGCGAGATTTAAACGGGGACGTGCGGCCAGAGCTGGGAA 360
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RESULT 13

US-08-834-497A-7
Sequence 7, Application US/08834497A
Patent No. 6140305

GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolf, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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US-08-834-497A-7

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Db	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGCTATGTGGAAGCAGAAATG	2400
QY	2401	AAGGAGCAACAGTAAAGAGCGGAGCCAGCAGGAAAGCTGTTACACAGTCCAGGCAAG	2460
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QY	2461	AGGTAGTGGAGTGGCTGGTGGGAACAGAAAAGGAGTGACAAACCAATTTGCTCCTGAA	2520
Db	2461	AGGTAGTGGAGTGGCTGGTGGGAACAGAAAAGGAGTGACAAACCAATTTGCTCCTGAA	2520
QY	2521	TATATTTCTGAAGGAATTTGCTGAAGGATTTCTATGTTGTGAGAGAAAGAAATTTGG	2580
Db	2521	TATATTTCTGAAGGAATTTGCTGAAGGATTTCTATGTTGTGAGAGAAAGAAATTTGG	2580
QY	2581	CTGGGTGTAGTACTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCTCTGAGCTCAGGA	2640
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Db	3121	TTGTTGGCTGAGGCAAGGTAGATCAATTTGAGGTCAAGGATTTTGAACAAGCTTGGCCACA	3180
QY	3181	TGGTGAACCCCATGTCTACTTAAATAACAAAAATTTAGCCTGGTGTGGCGCAGCGCT	3240
Db	3181	TGGTGAACCCCATGTCTACTTAAATAACAAAAATTTAGCCTGGTGTGGCGCAGCGCT	3240
QY	3241	ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGATCCCTTTGAACCCAGGAGGTGCAAG	3300
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Listing first 45 summaries

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SUMMARIES

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ALIGNMENTS

RESULT 1

US-10-138-888-1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497

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RESULT 2
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 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Winston J.
 ; Drayna, Dennis T.
 ; Feder, John N.
 ; Gnirke, Andreas
 ; Ruddy, David
 ; Tsuchihashi, Zenta
 ; Wolff, Roger K.
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/138,888
 ; FILING DATE: 02-May-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/834,497
 ; FILING DATE: 04-APR-1997
 ; APPLICATION NUMBER: US 08/652,265
 ; FILING DATE: 23-MAY-1996
 ; APPLICATION NUMBER: US 08/632,673
 ; FILING DATE: 16-APR-1996
 ; APPLICATION NUMBER: US 08/630,912
 ; FILING DATE: 04-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brian M. Poissant
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 8907-095-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; OTHER INFORMATION: /product= "Hereditary Hemochromatosis
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 ; gene 24d1 allele"
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Db 4801 AAATTCAGAAATGTCAAGCCGGGACGGTGGCTCACCCCTGTAATCCAGCACTTGG 4860
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Db 4861 AGCCGAGCGGGTGTGTCAAGAGTCAAGAGTTCAGACCCCTGACCAACATGGTGA 4920
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Db 4981 GCTAATTGGAAGCTGAGGC 5000
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|
|
```

RESULT 3

US-10-138-888-5

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Girke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888

FILING DATE: 02-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497

FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-MAY-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brian M. Poissant

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8907-095-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

OTHER INFORMATION: /product= "Hereditary Hemochromatosis
(HH) protein containing the 24d2
mutation"

/note= "Hereditary Hemochromatosis (HH)

Gene 24d2 allele"

FEATURE:

NAME/KEY: -

LOCATION: 140..7319

FEATURE:

NAME/KEY: -

LOCATION: 5507..6023

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-138-888-5

Query Match

Best Local Similarity 100.0%; Score 4998.4; DB 15; Length 10825;

Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	3001	GGACATGTTAAGTTTGTAGATTTCCAGTTCAGGCTTCCAAAGTGGTGTAGGCGCACATAGGCAGTT	3060
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Qy	3901		TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
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Db	4441		CTGGAGAGGACTGCGCTTCACAGCTGCAGAGTTCCTGGAGCTGGGGAGAGTGTTTTG	4500
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Qy	4561		AGGTTCCAGGGCAGGAATCCCTGGTTGAGTTTCAGAGGTGCTCAGGCTGTGCTCCTC	4620
Db	4561		AGGTTCCAGGGCAGGAATCCCTGGTTGAGTTTCAGAGGTGCTCAGGCTGTGCTCCTC	4620
Qy	4621		TCCAAATCTGGGAAGGACTTTTCTCAATCCTAGAGTCTCTACCTTATAATTCAGATGTA	4680
Db	4621		TCCAAATCTGGGAAGGACTTTTCTCAATCCTAGAGTCTCTACCTTATAATTCAGATGTA	4680
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Db	4681		TGAGACAGCCACAAGTCATGGGTTTAAATTTCTTTTCTCAATGATATGGCTCAAGGGAA	4740
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RESULT 4

US-10-138-888-7

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Girke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITY: New York
STREET: 1155 Avenue of the Americas
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864

OTHER INFORMATION: /product= "Hereditary Hemochromatosis
(HH) protein containing both the 24d1
and 24d2 mutations"

/note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"

FEATURE:

NAME/KEY: -
LOCATION: 140..7319
FEATURE:
NAME/KEY: -
LOCATION: 5507..6023
FEATURE:
NAME/KEY: allele
LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
(HH)"
/label= 24d1

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-138-888-7
Query Match 100.0%; Score 4998.4; DB 15; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCNATCAACACCCCT 120
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Db 121 TCAGGATTTAAAAACCAAGGGGGACACTGGATCACCTAGTGTGTTTCAAGCAGGTACCTT 180
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
Filing DATE: 02-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
Filing DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
Filing DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
Filing DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
Filing DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
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QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACGAGAGTT 240
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 Db 4501 GACCAACAAGGTATGTTGGAACACACTTCTGCCCCCTATCTAGTGGCAGAGTGGAG 4560
 QY 4561 AGTTTCAGGCAAGCAAGTCCCTGTTGAGTTTTCAGAGTGGCTGAGGCTGTGCTTC 4620
 Db 4561 AGTTTCAGGCAAGCAAGTCCCTGTTGAGTTTTCAGAGTGGCTGAGGCTGTGCTTC 4620
 QY 4621 TCCAAATTCGGGAAGGACTTCTCAATCCTAGAGTCTTACCTTATATATGAGATGA 4680
 Db 4621 TCCAAATTCGGGAAGGACTTCTCAATCCTAGAGTCTTACCTTATATATGAGATGA 4680
 QY 4681 TGAGACAGCACAAGTATGAGGTTTAAATTTCTTTTCTCCATGATATGCTCAAGAGGAA 4740
 Db 4681 TGAGACAGCACAAGTATGAGGTTTAAATTTCTTTTCTCCATGATATGCTCAAGAGGAA 4740
 QY 4741 GTGTCTATGGCCCTTCTTTTATTTAAACAATATCTTTTGTATATTTATACCTGTTAA 4800
 Db 4741 GTGTCTATGGCCCTTCTTTTATTTAAACAATATCTTTTGTATATTTATACCTGTTAA 4800

QY 4801 AAATTCAGAAATGTCAAGCCGGGACCGGTGGCTACCCCTGTAAATCCAGCACTTTGGG 4860
 Db 4801 AAATTCAGAAATGTCAAGCCGGGACCGGTGGCTACCCCTGTAAATCCAGCACTTTGGG 4860
 QY 4861 AGGCCGAGCGGGTGTGTCAAGGTCAGGAGTTTGAGACCGCTGACCAACATGTGAA 4920
 Db 4861 AGGCCGAGCGGGTGTGTCAAGGTCAGGAGTTTGAGACCGCTGACCAACATGTGAA 4920
 QY 4921 ACCCGTCTCTAAATAATCAAAAATAGCTGGTACAGTCACTGCGCACTGTAGTCCCA 4980
 Db 4921 ACCCGTCTCTCTAAATAATCAAAAATAGCTGGTACAGTCACTGCGCACTGTAGTCCCA 4980
 QY 4981 GCTAATTTGGAAGCTGAGGC 5000
 Db 4981 GCTAATTTGGAAGCTGAGGC 5000

RESULT 6

US-10-301-844-1/c
 ; Sequence 1, Application US/10301844
 ; Publication No. US20030100747A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruddy, David A.
 ; ; Wolff, Roger K.
 ; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
 ; ; HEMOCHROMATOSIS GENE
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds, LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/301,844
 ; FILING DATE: 20-No. US20030100747A1-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/852,495C
 ; FILING DATE: 07-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Poissant, Brian M
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 8907-0057-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235033 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-301-844-1

Query Match 99.8%; Score 4988; DB 15; Length 235033;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4999; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 TCTAGGTTGAGATAAATTTTAAATCTATGATGAAATTTTGAATCAATAATTTTA 60
 Db 47148 TCTAGGTTGAGATAAATTTTAAATCTATGATGAAATTTTGAATCAATAATTTTA 47089
 QY 61 AATATCTAAAGTTTCAGATCAGAAACATTCGGAAGCTACTTTCCCAATCAACACCCCT 120

[illegible]

Db	46008	CTAGGCTTTATTGATTTGGCAATGCTGTGTAAATTAAGAGGGCCTCTCTACAAGTACTGA	45949
Qy	1201	TAATGAACATGTAAAGCAATGCACCTCACTTCTAAAGTTTACATTCATATCTCATTTATTTGA	1260
Db	45948	TAATGAACATGTAAAGCAATGCACCTCACTTCTAAAGTTTACATTCATATCTCATTTATTTGA	45889
Qy	1261	TTTTTCACTAGGCATAGGAGGTTAGGAGCTAAATAACGTTTTATTTTACTPAGAAGTTAACT	1320
Db	45988	TTTTTCACTAGGCATAGGAGGTTAGGAGCTAAATAACGTTTTATTTTACTPAGAAGTTAACT	45829
Qy	1321	GGAAATTCAGATTATATACTCTTTTTCAGGTTACAAAGAACATAATAATCTCGTTTTCTG	1380
Db	45828	GGAAATTCAGATTATATACTCTTTTTCAGGTTACAAAGAACATAATAATCTCGTTTTCTG	45769
Qy	1381	ATGTATATTTTCAAGTACTACAGCTGCTTTAACTCTTAGTTGACAGTGAATTTCCGCCCTGTAG	1440
Db	45768	ATGTATATTTTCAAGTACTACAGCTGCTTTAACTCTTAGTTGACAGTGAATTTCCGCCCTGTAG	45709
Qy	1441	TGTAGCACAGTGTCTGTGGGTACACGCGCGGCTCAGCACAGCACTTTTGAGTTTGGTGA	1500
Db	45708	TGTAGCACAGTGTCTGTGGGTACACGCGCGGCTCAGCACAGCACTTTTGAGTTTGGTGA	45649
Qy	1501	CTACGTGTATCCACATTTTACACATGACAAAGAAATGAGGCATGGCAGCGCTCCTCTGG	1560
Db	45648	CTACGTGTATCCACATTTTACACATGACAAAGAAATGAGGCATGGCAGCGCTCCTCTGG	45589
Qy	1561	CAAAATTTTCAATGTGACACTGGGCTTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
Db	45588	CAAAATTTTCAATGTGACACTGGGCTTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	45529
Qy	1621	TATGATTTCTTAAACATCACATGTCATTAGAGGTTGAAATAATAAATTTTCATGTTGAGCAG	1680
Db	45528	TATGATTTCTTAAACATCACATGTCATTAGAGGTTGAAATAATAAATTTTCATGTTGAGCAG	45469
Qy	1681	AAATAATTCATGTTTACAGTGTAAATGATGCCAGCCATGTGTGCACTGTTTCAAGCCC	1740
Db	45468	AAATAATTCATGTTTACAGTGTAAATGATGCCAGCCATGTGTGCACTGTTTCAAGCCC	45409
Qy	1741	CAAGGAGAGAGCAGAGGAAACAAGTCTTTTACCCCTTTGATATTTTGCATTTAGTGGGAGA	1800
Db	45408	CAAGGAGAGAGCAGAGGAAACAAGTCTTTTACCCCTTTGATATTTTGCATTTAGTGGGAGA	45349
Qy	1801	GATGACAAATTAAGCAAAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA	1860
Db	45348	GATGACAAATTAAGCAAAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA	45289
Qy	1861	GAAGCAGAGAAGTTCAGGCGAAGTCACTCTGGGCTGACACTTGGAGCAGAGACATGAAGA	1920
Db	45288	GAAGCAGAGAAGTTCAGGCGAAGTCACTCTGGGCTGACACTTGGAGCAGAGACATGAAGA	45229
Qy	1921	AATAAGAAATCATATTCAGCTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTCGCAG	1980
Db	45228	AATAAGAAATCATATTCAGCTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTCGCAG	45169
Qy	1981	TTTGATTTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	2040
Db	45168	TTTGAATTTAAAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	45109
Qy	2041	CGGCGTGGGGTGGGAAGGGGGACTACCAATCTGATGTAGGATGTCTAGCAGTATCTGT	2100
Db	45108	CGGCGTGGGGTGGGAAGGGGGACTACCAATCTGATGTAGGATGTCTAGCAGTATCTGT	45049
Qy	2101	CCCTCCCTACTCATCTAGGTGCTAGGAGCACTCCCCAGTCTTCACAAACCAAAATGTCTCT	2160
Db	45048	CCCTCCCTACTCATCTAGGTGCTAGGAGCACTCCCCAGTCTTCACAAACCAAAATGTCTCT	44989
Qy	2161	AAACTTTGGCCACATGTCACTTAGTAGCAAACTCTCTGGTTAAGAAGCTCGGGTTGAAAA	2220
Db	44988	AAACTTTGGCCACATGTCACTTAGTAGCAAACTCTCTGGTTAAGAAGCTCGGGTTGAAAA	44929
Qy	2221	AATAAACAAAGTGTGTGGGGAGTAGAGGCCAAGAAATAGGTAATGGGCTCAGAGAGA	2280
Db	44928	AATAAACAAAGTGTGTGGGGAGTAGAGGCCAAGAAATAGGTAATGGGCTCAGAGAGA	44869

SEQUENCE CHARACTERISTICS:

LENGTH: 237326 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-301-844-2

Query Match	99.2%;	Score	4958.8;	DB	15;	Length	237326;
Best Local Similarity	99.8%;	Pred. No.	0;				
Matches	4996;	Conservative	0;	Mismatches	2;	Indels	6;
						Gaps	3;
QY	1	TCTAAGGTTGAGATAAAATTTTAAATGATATGAAATTTTGAATAATCATAAATATTTA	60				
DB	47101	TCTAAGGTTGAGATAAAATTTTAAATGATATGAAATTTTGAATAATCATAAATATTTA	47042				
QY	61	AATATCTAAGTTCAGATCAGACATTCGGAAGCTACTTTCCCAATCAACAACCCCT	120				
DB	47041	AATATCTAAGTTCAGATCAGACATTCGGAAGCTACTTTCCCAATCAACAACCCCT	46982				
QY	121	TCAGGATTTAAACCAAGGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT	180				
DB	46981	TCAGGATTTAAACCAAGGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT	46922				
QY	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGTGCTTTTCCACGAGAGTT	240				
DB	46921	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGTGCTTTTCCACGAGAGTT	46862				
QY	241	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGCTGACTCTGAGGCATCCCG	300				
DB	46861	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGCTGACTCTGAGGCATCCCG	46802				
QY	301	TTTCCCGCCGCCCAAGGAGAGGAGATTTAAACGGGGACGTGCGGCAGAGCTGGGGAA	360				
DB	46801	TTTCCCGCCGCCCAAGGAGAGGAGATTTAAACGGGGACGTGCGGCAGAGCTGGGGAA	46742				
QY	361	ATGGGCGCGAGCCAGCCGCGCTTCTCCTGATGCTTTTGACAGCCGCGTCTTG	420				
DB	46741	ATGGGCGCGAGCCAGCCGCGCTTCTCCTGATGCTTTTGACAGCCGCGTCTTG	46682				
QY	421	CAGGGCGCTTCTGCTGAGTCCGAGGGCTCGGGCGAACTAGGGGCGCGCGGGGTG	480				
DB	46681	CAGGGCGCTTCTGCTGAGTCCGAGGGCTCGGGCGAACTAGGGGCGCGCGGGGTG	46622				
QY	481	GAATAATCGAACTAGCTTTTCTTTGCGCTTGGAGTTTGCTTAATTTGGAGGACCTGC	540				
DB	46621	GAATAATCGAACTAGCTTTTCTTTGCGCTTGGAGTTTGCTTAATTTGGAGGACCTGC	46562				
QY	541	TCACCCCTATCCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC	600				
DB	46561	TCACCCCTATCCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC	46502				
QY	601	CTACCACTGAATCGAGATAGGGTCCCTGCGCCCGAGACTGCGCCCTCCCGCGCTGT	660				
DB	46501	CTACCACTGAATCGAGATAGGGTCCCTGCGCCCGAGACTGCGCCCTCCCGCGCTGT	46442				
QY	661	CCCGGCTCTGCGAGTGACTTTTGAACCGCCACTCCCTTCCGCCCACTAGAATGCTTT	720				
DB	46441	CCCGGCTCTGCGAGTGACTTTTGAACCGCCACTCCCTTCCGCCCACTAGAATGCTTT	46382				
QY	721	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTTAAGCTGGGGCTCTTTGAACCTGG	780				
DB	46381	TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTTAAGCTGGGGCTCTTTGAACCTGG	46322				
QY	781	AACTCGGGTTATTTCCCAATGTCAGCTGTGAGTTTTCCTCCAGTCATCTCCAAACAGG	840				
DB	46321	AACTCGGGTTATTTCCCAATGTCAGCTGTGAGTTTTCCTCCAGTCATCTCCAAACAGG	46262				
QY	841	AAAGTCTTCCCTGAGTGTCTGCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	900				
DB	46261	AAAGTCTTCCCTGAGTGTCTGCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	46202				
QY	901	GGTTTCCACCTCAGAACGAATGCGTTGGGCGGTGGGGCGCGGAAGAGTGGCGTTGGGGA	960				

DB	46201	GGTTTCCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGGAAGAGTGGCGTTGGGGA	46142				
QY	961	TCTGAATTTCTTCCACCATTTCCACCCACTTTTGGTGAGACTGGGGTGAGGCTCTTAGGGT	1020				
DB	46141	TCTGAATTTCTTCCACCATTTCCACCCACTTTTGGTGAGACTGGGGTGAGGCTCTTAGGGT	46082				
QY	1021	GGGAGGCTCTCAGAGAGAGCCCTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080				
DB	46081	GGGAGGCTCTCAGAGAGAGCCCTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	46022				
QY	1081	GCTCGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACAAATTTCTCTTTTCGG	1140				
DB	46021	GCTCGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACAAATTTCTCTTTTCGG	45962				
QY	1141	CTAGGCTTTATGATTTGCAATGCTGTGTAATTTAAGAGGCTCTCTCAAGACTACTGA	1200				
DB	45961	CTAGGCTTTATGATTTGCAATGCTGTGTAATTTAAGAGGCTCTCTCAAGACTACTGA	45902				
QY	1201	TAATGAAACATGTAAGCAATGCACTCACTTCTAAGTTTACATTCATATCTGATTTTGA	1260				
DB	45901	TAATGAAACATGTAAGCAATGCACTCACTTCTAAGTTTACATTCATATCTGATTTTGA	45842				
QY	1261	TTTTCACTAGGCATAGGAGGTAGAGCTTAATAACGTTTATTTTACTAGAAGTTAACT	1320				
DB	45841	TTTTCACTAGGCATAGGAGGTAGAGCTTAATAACGTTTATTTTACTAGAAGTTAACT	45782				
QY	1321	GGAAATTCAGATTTATTAATCTCTTTTCAAGTTTCAAGAACATAAATAATCTGGTTCTG	1380				
DB	45781	GGAAATTCAGATTTATTAATCTCTTTTCAAGTTTCAAGAACATAAATAATCTGGTTCTG	45722				
QY	1381	ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTGTAGTTGACAGTGAATTTGCCCTGTAG	1440				
DB	45721	ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTGTAGTTGACAGTGAATTTGCCCTGTAG	45662				
QY	1441	TGTAGCAGAGTGTCTGTGGGTCAACCGCGGCTTCAGCACAGCACTTTGAGTTTGTGTA	1500				
DB	45661	TGTAGCAGAGTGTCTGTGGGTCAACCGCGGCTTCAGCACAGCACTTTGAGTTTGTGTA	45602				
QY	1501	CTACGCTATCCACATTTTACATGACAGAAATGAGCAGTGGCAGCGGCTGCTTCTG	1560				
DB	45601	CTACGCTATCCACATTTTACATGACAGAAATGAGCAGTGGCAGCGGCTGCTTCTG	45542				
QY	1561	CAAAATTTTCAATGCTACCTGCGCTTTGGTGGCAGAGCTCATGCTCCACTTCATAGC	1620				
DB	45541	CAAAATTTTCAATGCTACCTGCGCTTTGGTGGCAGAGCTCATGCTCCACTTCATAGC	45482				
QY	1621	TATGATTTCTTAAACATCACTGCAATTAGAGTTGAATAATAAATTTCAATGTTGAGCAG	1680				
DB	45481	TATGATTTCTTAAACATCACTGCAATTAGAGTTGAATAATAAATTTCAATGTTGAGCAG	45422				
QY	1681	AAATATTTCAATTTTACAAAGTGAATGAGTCCCGAGCAGTGTGTCAGCTGTTCAAGCCC	1740				
DB	45421	AAATATTTCAATTTTACAAAGTGAATGAGTCCCGAGCAGTGTGTCAGCTGTTCAAGCCC	45362				
QY	1741	CAAGGAGAGAGCAGGAGAAACAAGTCTTTACCTTTTGTATTTTGCATTTCTAGTGGGAGA	1800				
DB	45361	CAAGGAGAGAGCAGGAGAAACAAGTCTTTTACCTTTTGTATTTTGCATTTCTAGTGGGAGA	45302				
QY	1801	GATGCAATAAGCAAAATGAGCAGAAAGATATACAACTACAGGAAATCATGGGTGTTGTA	1860				
DB	45301	GATGCAATAAGCAAAATGAGCAGAAAGATATACAACTACAGGAAATCATGGGTGTTGTA	45242				
QY	1861	GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTGACGAGACATCAAGGA	1920				
DB	45241	GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTGACGAGACATCAAGGA	45182				
QY	1921	AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTCGGCAAG	1980				
DB	45181	AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTCGGCAAG	45122				
QY	1981	TTGATTTAAAGCGGGTTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG	2040				

Db	45121	TTGATTTAAAGAGCGGGTTTTCTCAGCACTTACTCATGTGTGTGTGTGT- GGSGGGGGGGGG	45063
Qy	2041	CGGCGTGGGGTGGAAGAGGGGACCTACCATCTGCATGTAGGATGTCTAGCACGTATCCCTGT	2100
Db	45062	CGGCGTGGGGTGGAAGAGGGGACTACCATCTGCATGTAGGATGTCTAGCACGTATCCCTGT	45003
Qy	2101	CCTCCCTACTCATCTAGTGTCTAGGAGCACTCCCCAGTCCTTGACAACCAAAAATGTCTCT	2160
Db	45002	CCTCCCTACTCATCTAGTGTCTAGGAGCACTCCCCAGTCCTTGACAACCAAAAATGTCTCT	44943
Qy	2161	AAACTTTGCCACATGTCACCTAGTAGACAAAATCTCTGGTTAAGAAGCTCGGTTGAAAA	2220
Db	44942	AAACTTTGCCACATGTCACCTAGTAGACAAAATCTCTGGTTAAGAAGCTCGGTTGAAAA	44883
Qy	2221	AATAAACAACTAGTGTGGGAGTAGAGGCCAAGAAGTAGGTAAATGGGCTCAGAAAGGA	2280
Db	44882	AATAAACAACTAGTGTGGGAGTAGAGGCCAAGAAGTAGGTAAATGGGCTCAGAAAGGA	44823
Qy	2281	GCCACAAACAAAGTTGTGCAGGGCCCTGTAGGCTGTGGTGTGAATTTAGCCAAGGAGTA	2344
Db	44822	GCCACAAACAAAGTTGTGCAGGGCCCTGTAGGCTGTGGTGTGAATTTAGCCAAGGAGTA	44763
Qy	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGACGAATG	2400
Db	44762	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAAGACGAATG	44703
Qy	2401	AAGGGACCAACAGTAAAGACAGGAGCCCAGCCAGGAAGCTGTATACACAGTCCAGGCAAG	2460
Db	44702	AAGGGACCAACAGTAAAGACAGGAGCCCAGCCAGGAAGCTGTATACACAGTCCAGGCAAG	44643
Qy	2461	AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAAAGGAGTGACAAAACATTTGCTCTGAA	2520
Db	44642	AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAAAGGAGTGACAAAACATTTGCTCTGAA	44583
Qy	2521	TATATTTGAAGGAAGTTGTGAAGGATTTATGTTGTGTGAGAGAAAGAGAAGTAATGG	2580
Db	44582	TATATTTGAAGGAAGTTGTGAAGGATTTATGTTGTGTGAGAGAAAGAGAAGTAATGG	44523
Qy	2581	CTGGGTGCTAGTACTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	2640
Db	44522	CTGGGTGCTAGTACTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA	44463
Qy	2641	GTTCAAGACCAGCCTGGGCAACACAGCAAACCCCTTCTTACAAAAATACAAAAATTA	2700
Db	44462	GTTCAAGACCAGCCTGGGCAACACAGCAAACCCCTTCTTACAAAAATACAAAAATTA	44403
Qy	2701	GCTGGGTGTGGTGGCATGCACTGTGANTCTAGCTACTCGGGAGGCTGAGGTGZAGGTA	2760
Db	44402	GCTGGGTGTGGTGGCATGCACTGTGANTCTAGCTACTCGGGAGGCTGAGGTGZAGGTA	44343
Qy	2761	TTGCTTCAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTCTCAGC	2820
Db	44342	TTGCTTCAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTCTCAGC	44283
Qy	2821	CTAGGTGCACAGACCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAGTAGTTAAAGT	2880
Db	44282	CTAGGTGCACAGACCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAGTAGTTAAAGT	44223
Qy	2881	TGACTTTGTCTTTATTTTAAATTTTATGCGCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
Db	44222	TGACTTTGTCTTTATTTTAAATTTTATTTGGCTGTAGCAGTGGGGTAAATTTGGCAATGCCAT	44163
Qy	2941	TTCTGAGATGGTGAAGCAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTTG	3000
Db	44162	TTCTGAGATGGTGAAGCAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTT-	44104
Qy	3001	GGACATGTTAAGTTTGAAGTTTCCAGTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	44103	GGACATGTTAAGTTTGAAGTTTCCAGTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT	44044
Qy	3061	CAGTGTGAAGAAATTCAGAACCAAGGCTGGGCA CGGTGGCTCACCTTCTGTAATCCCGCACT	3120
Db	44043	CAGTGTGAAGAAATTCAGAACCAAGGCTGGGCA CGGTGGCTCACCTTCTGTAATCCCGCACT	43984

[illegible]

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QY 4197 CTTTGGTGTGAGTAAACAGGCTGGGGATTTTTCAGAGTCCACACCTCGAGTCAAT 4256
Db 42903 CTTTGGTGTGAGTAAACAGGCTGGGGATTTTTCAGAGTCCACACCTCGAGTCAAT 42844
QY 4257 CTGGGGCTGTGAATACCAAGACACACAGTACCGAGGGCTACTGGAAGTACGGGTATGA 4316
Db 42843 CTGGGGCTGTGAATACCAAGACACACAGTACCGAGGGCTACTGGAAGTACGGGTATGA 42784
QY 4317 TGGGACAGGACCACTTTGAATTTCTGCCCTGCACACATCTGGATTTGGAGACGACGAAACCCAG 4376
Db 42783 TGGGACAGGACCACTTTGAATTTCTGCCCTGCACACATCTGGATTTGGAGACGACGAAACCCAG 42724
QY 4377 GGCCTGCCCAACAAGCTGGAGTGGGAAGGACACAAGATTCGGGCCAGGACGAGGCG 4436
Db 42723 GGCCTGCCCAACAAGCTGGAGTGGGAAGGACACAAGATTCGGGCCAGGACGAGGCG 42664
QY 4437 CTACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGAGAGGTGT 4496
Db 42663 CTACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGAGAGGTGT 42604
QY 4497 TTTGGACCAACAGGTATGGTGGAAACACACTTCTGCCCTATACCTCTAGTGGCAGAGTG 4556
Db 42603 TTTGGACCAACAGGTATGGTGGAAACACACTTCTGCCCTATACCTCTAGTGGCAGAGTG 42544
QY 4557 GAGGAGGTTGACGGGCAACGGAATCCCTGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTG 4616
Db 42543 GAGGAGGTTGACGGGCAACGGAATCCCTGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTG 42484
QY 4617 CTTCTCCAAATTCGGGAAGGACCTTCTCAATCCTAGAGTCTCTACCTTATAATGAGA 4676
Db 42483 CTTCTCCAAATTCGGGAAGGACCTTCTCAATCCTAGAGTCTCTACCTTATAATGAGA 42424
QY 4677 TGTATGAGACAGCACAAGTCAATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAG 4736
Db 42423 TGTATGAGACAGCACAAGTCAATGGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAG 42364
QY 4737 GGAAGTGTCTATGGCCCTTGCTTTTATTAACCAATAATCTTTTGTATATTTATACCTG 4796
Db 42363 GGAAGTGTCTATGGCCCTTGCTTTTATTAACCAATAATCTTTTGTATATTTATACCTG 42304
QY 4797 TTAATAATTCAGAAATGTCAAGCCGGGACCGTGGCTCACCCCTGTATATCCAGCACTT 4856
Db 42303 TTAATAATTCAGAAATGTCAAGCCGGGACCGTGGCTCACCCCTGTATATCCAGCACTT 42244
QY 4857 TGGGAGGCGGAGCGGGTGGTCAACAGGTTCAGAGTTCAGACACGCTGACCAACATGG 4916
Db 42243 TGGGAGGCGGAGCGGGTGGTCAACAGGTTCAGAGTTCAGACACGCTGACCAACATGG 42184
QY 4917 TGAAACCCGCTCTTAAAAAATACAAAAATTAGCTGGTCAAGTCAATGCGCACTGTAGT 4976
Db 42183 TGAAACCCGCTCTTAAAAAATACAAAAATTAGCTGGTCAAGTCAATGCGCACTGTAGT 42124
QY 4977 CCCAGCTAATTCGAAGGCTGAGGC 5000
Db 42123 CCCAGCTAATTCGAAGGCTGAGGC 42100
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RESULT 9
US-09-981-606-27
; Sequence 27, Application US/09981606
; Publication NO. US20030129595A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TITLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT APPLICATION NUMBER: US/09/981,606
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 12146
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-606-27

Query Match 99.1%; Score 4957.2; DB 10; Length 12146;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4995; Conservative 0; Mismatches 3; Indels 6; Gaps 3;

QY 1 TCTAAGTTGAGATATAATTTTAAATGTATGATTTGAAATTTTGAATAATCATATAATTATTA 60
Db 889 TCTAAGTTGAGATATAATTTTAAATGTATGATTTGAAATTTTGAATAATCATATAATTATTA 948
QY 61 AATATCTAAAGTTTCAGATCAGAAACATTCGAAAGTACTTTTCCCAATCAACACACCCCT 120
Db 949 AATATCTAAAGTTTCAGATCAGAAACATTCGAAAGTACTTTTCCCAATCAACACACCCCT 1008
QY 121 TCAGGATTTAAATAACCAAGGGGACACTGGATCACTAGTGTTCACAAGAGGATACCTT 180
Db 1009 TCAGGATTTAAATAACCAAGGGGACACTGGATCACTAGTGTTCACAAGAGGATACCTT 1068
QY 181 CTGCTGTAGGACAGAGAGAACTAAAGTTCTGAAAGACCTGTGTGCTTTTCCACGAGGAATT 240
Db 1069 CTGCTGTAGGACAGAGAGAACTAAAGTTCTGAAAGACCTGTGTGCTTTTCCACGAGGAATT 1128
QY 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGCTGACTTCTGAGAGCCATCCCCG 300
Db 1129 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGCTGACTTCTGAGAGCCATCCCCG 1188
QY 301 TTTCCCGCGCCCCCAAAAAGAGCGGAGATTTAACGGGGACGTCGGCCAGAGCTGGGGAA 360
Db 1189 TTTCCCGCGCCCCCAAAAAGAGCGGAGATTTAACGGGGACGTCGGCCAGAGCTGGGGAA 1248
QY 361 ATGGCCCGCGCAGCAGCGCGCTCTCTCTCTGATGCTTTTGCAGACCGCGGTCTG 420
Db 1249 ATGGCCCGCGCAGCAGCGCGCTCTCTCTCTGATGCTTTTGCAGACCGCGGTCTG 1308
QY 421 CAGGGCGCGCTGCTCGTGAAGTCCGAGGGCTCGCGGCGAACTAGGGGCGCGCGGGGTG 480
Db 1309 CAGGGCGCGCTGCTCGTGAAGTCCGAGGGCTCGCGGCGAACTAGGGGCGCGCGGGGTG 1368
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTTGGAGTTTGTCTAACTTTGGAGGACCTGC 540
Db 1369 GAAAAATCGAAACTAGCTTTTCTTTGGCTTTGGAGTTTGTCTAACTTTGGAGGACCTGC 1428
QY 541 TCACCCCTATCCGAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 1429 TCACCCCTATCCGAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1488
QY 601 CTACCACTGAATCGAGATAGGGGTCTCTCGCCCGAGGACCTGCCCCCTTCCCGGCTGT 660
Db 1489 CTACCACTGAATCGAGATAGGGGTCTCTCGCCCGAGGACCTGCCCCCTTCCCGGCTGT 1548
QY 661 CCCGCTCTGGGAGTGACTTTTGGAAACCGGCCACTCCCTTCCCGCAACTAGAAATGCTTT 720
Db 1549 CCCGCTCTGGGAGTGACTTTTGGAAACCGGCCACTCCCTTCCCGCAACTAGAAATGCTTT 1608
QY 721 TAAATAAATCTGTAGTTCTCTCAATGTGAGTTTTCAGAGTTTTCAGAGTTTTCAGAGTTT 780
Db 1609 TAAATAAATCTGTAGTTCTCTCAATGTGAGTTTTCAGAGTTTTCAGAGTTTTCAGAGTTT 1668
QY 781 AACTCGGGTTTATTTTCAATGTGAGTTTTCAGAGTTTTCAGAGTTTTCAGAGTTTTCAGAG 840
Db 1669 AACTCGGGTTTATTTTCAATGTGAGTTTTCAGAGTTTTCAGAGTTTTCAGAGTTTTCAGAG 1728
QY 841 AAGTTCTTCTGAGTGTCTGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900
Db 1729 AAGTTCTTCTGAGTGTCTGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 1788
QY 901 GGTTCACACCTCAGAACGAATCGGTGGGGCGGCGGAGAGTGGGTGGGGA 960
Db 1789 GGTTCACACCTCAGAACGAATCGGTGGGGCGGCGGAGAGTGGGTGGGGA 1848
QY 961 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGTGTAGACCTTGGGGTGGAGGTCTCTAGGT 1020
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[illegible]

Db	2928	CGGCGTGGGGGTGGGAAAGGGGGA	CTACCA	TCTGCATGTAGGATGTCTAGCAGTATCCTCTG	298
Qy	2101	CCTCCCTACTCACTAGTGTCTAGGAG	CAC	TCCCCCAGTCTTTGACAACCAAAAAATGTCCT	2160
Db	2988	CCTCCCTACTCACTAGTGTCTAGGAG	CACTCCCCCAGTCTTTGACAACCAAAAAATGTCCT	3047	
Qy	2161	AAACTTTGCCACATGTCACTAGT	AGCAAACTCTCTGGTTTAAAGCTCGGGTTGAAAA	2220	
Db	3048	AAACTTTGCCACATGTCACTAGT	AGCAAACTCTCTGGTTTAAAGCTCGGGTTGAAAA	3107	
Qy	2221	AATAAACAAGTAGTGTGGGGAGT	AGAGCCAGAGTAGGTAAATGGGCTCAGAAAGGA	2280	
Db	3108	AATAAACAAGTAGTGTGGGGAGT	AGAGCCAGAGTAGGTAAATGGGCTCAGAAAGGA	3167	
Qy	2281	GCCACAAA	CAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATTTCTAGCCCAAGAGTA	2340	
Db	3168	GCCACAAA	CAAGGTTGTGCAGGCGCCTGTAGGCTGTGGTGTGAATTTCTAGCCCAAGAGTA	3227	
Qy	2341	ACAGTGATCTGTCA	CAGGCTTTTAAAAAGATTGCTCTGGCTGTATGTGGAAGACGAAATG	2400	
Db	3228	ACAGTGATCTGTCA	CAGGCTTTTAAAAAGATTGCTCTGGCTGTATGTGGAAGACGAAATG	3287	
Qy	2401	AAGGGACCAACAGTAA	AAGCAGGAGGCCAGCCAGGAGAGCTGTATACACAGTCCAGGCAAG	2460	
Db	3288	AAGGGACCAACAGTAA	AAGCAGGAGGCCAGCCAGGAGAGCTGTATACACAGTCCAGGCAAG	3347	
Qy	2461	AGGTAGTGGAGTGGGCTGGGAT	GGGACAGAAAAAGGAGTGCACAAACATTGTCTCTCTGAA	2520	
Db	3348	AGGTAGTGGAGTGGGCTGGGAT	GGGACAGAAAAAGGAGTGCACAAACATTGTCTCTCTGAA	3407	
Qy	2521	TATATTTCTGAAGAAAGTTGCT	GAAAGTTCATATGTTGTGTGAGAGAAAGAGAAATTTGG	2580	
Db	3408	TATATTTCTGAAGAAAGTTGCT	GAAAGTTCATATGTTGTGTGAGAGAAAGAGAAATTTGG	3467	
Qy	2581	CTGGGTGTAGTAC	TCAATGCAAGAGAGAGGCCAAGGAGAGCAGATTTCTGAGCTCAGGA	2640	
Db	3468	CTGGGTGTAGTAC	TCAATGCAAGAGAGAGGCCAAGGAGAGCAGATTTCTGAGCTCAGGA	3527	
Qy	2641	GTTCACAGACAGCCTGGGCA	CAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700	
Db	3528	GTTCACAGACAGCCTGGGCA	CAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	3587	
Qy	2701	GCTGGGTGTGGTGGCATGCA	CCCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA	2760	
Db	3588	GCTGGGTGTGGTGGCATGCA	CCCTGTGATCCTAGCTACTCGGGAGGCTGAGGTGGAGGTA	3647	
Qy	2761	TTGCTTGAGCCCAAGGAAGTTG	AGCGCTGCAGTGCACATGACTGTGCGCATCTGTACTTTCAGC	2820	
Db	3648	TTGCTTGAGCCCAAGGAAGTTG	AGCGCTGCAGTGCACATGACTGTGCGCATCTGTACTTTCAGC	3707	
Qy	2821	CTAGGTACAGACAGACACCC	CTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT	2880	
Db	3708	CTAGGTACAGACAGACACCC	CTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT	3767	
Qy	2881	TGACTTTTGTCTTTATTTTAA	TTTTTATTTGSCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940	
Db	3768	TGACTTTTGTCTTTATTTTAA	TTTTTATTTGSCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	3827	
Qy	2941	TTCTGAGATGGTGAAGCAGAG	GAAGACAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000	
Db	3828	TTCTGAGATGGTGAAGCAGAG	GAAGACAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG	3886	
Qy	3001	GGACATGTTAAGTTTGAGAT	TCCAGTCCAGGCTTCCAAAGTGGTGCAGGCCACATAGGCAGTT	3060	
Db	3887	GGACATGTTAAGTTTGAGAT	TCCAGTCCAGGCTTCCAAAGTGGTGCAGGCCACATAGGCAGTT	3946	
Qy	3061	CAGTGTAAAGAAATTCAGGAC	CAAGGCTGGGCACGGTGGCTCAC	TCTGTATCTCCAGCACT	3120
Db	3947	CAGTGTAAAGAAATTCAGGAC	CAAGGCTGGGCACGGTGGCTCAC	TCTGTATCTCCAGCACT	4006
Qy	3121	TTGTGTGCTGAGGCAGGTTAG	ATCATTTGAGGTGAGGATTTTGAGACAGCTTGCCCAACA	3180	
Db	4007	TTGTGTGCTGAGGCAGGTTAG	ATCATTTGAGGTGAGGATTTTGAGACAGCTTGCCCAACA	4066	

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2501 TTTTCACTAAACATAAAAAATAAAAACTAAATAATACGTTTATTTTACTAAAAAATAAAT 2442
1321 GGAATTCAGATTATATAAATCTTTTTCAGGTTTCAAAAGAACATAAATAATCTGGTTTCTG 1380
2441 AANATTCAAATTAATATACTCTTTTCAATTAACAAAACATAAATAATCTAATTTTCTA 2382
1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTTAGTTGACAGTGAATTTGCGCTGTAG 1440
2381 ATATTAATTTCAAACTACTACAACTACTTCTAATCTTAATTAACAAATAATTTTACCCTATAA 2322
1441 TGTAGCACAGTGTCTGTGGGTACACGCGCGCTCAGCACAGCACCTTTGAGTTTGGTA 1500
2321 TATAACACAATAATTTTATAAATCACACGCGGCTCAACACACACCTTTTAAATTTTAAATA 2262
1501 CTACGTGTATCCACATTTTACACATGACCAAGATGAGGATGCGCGCTGCTCCTCG 1560
2261 CTACGTATATCCCATTTTACACATGACCAAAATAAATAAATAACACAGCTACTTCTCTAA 2202
1561 CAAATTTATTCATGTTGCTGGCTTTGTTGGCGAGCTCATGTCTCCACTTTCATAGC 1620
2201 CAAATTTATTCATATAACATCACTAACTTTAATAACAAAACCTCATATCTCCACTTCATAAC 2142
1621 TATGATTTTAAACATCACTGCTATAGAGTTGAATTAATAAATTTTATGTTGAGCAG 1680
2141 TATAATTTCTTAAACATCACTACATTAATAAATAAATAAATAAATAAATTTTCAATAAC 2082
1681 AAATATTTCAATGTTTACAAGTGTAAATGATGCCAGCCATGTTGTCACCTGTTCAAGCCC 1740
2081 AAATATTTCAATTTTACAATAATAAATAAATCCCAACCATATATACATATTTCAAAACC 2022
1741 CAAGGAGAGAGCAGGGAACCAAGTCTTTACCTTTTGATTTTGTATTTCTAGTGGAGA 1800
2021 CAAAAAATAAACAACAAATCTTTACCTTTTAAATTTTACATTTCTAATAAAAA 1962
1801 GATGACAATAAGCAATAGCAGAAAGATATACAACTCAGGAAATCATGGGTGTTGTA 1860
1961 AATAACAATAAACAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1902
1861 GAAGCAGAGAAGTCAGGCAAGTCACCTCTGGGCTGACACTTTGAGCAGAGACATGAGGA 1920
1901 AAAAAAATAAACAACAAATCACTTAAACCTAAACCTTAAACAAAACATAAAAA 1842
1921 AATAAGAATGATATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
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1981 TTGGATTAAAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
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1661 CCTCCCTACTACTAATAACTAATAAACACTCCCGCAATCTTAACCAACCAAAATATCTCT 1602
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1541 AATAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1482
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1481 ACCAACAACAATAATATACAAAGCGCTATAAATCTAATAAATAAATTTCTAACCATAAATA 1422
2341 ACAGTGATCTGCACAGGCTTTTAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAAATG 2400

1421 ACAATAATCTATCACAAACTTTTAAAAAATTACTCTAACTACTATATAAAAAACAATA 1362
2401 AAGGAGCAACAGTAAAAAGCAGGAGCCAGCAGCAAGCTGTTCACAGTCTCAGGCAAG 2460
1361 AAAAAACCAACATTAATAAACAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1302
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3001 GGACATGTTAAGTTTGTAGATTTCCAGTCTCAGGCTTCCAGTGGTGGGCGCACATAGGAGT 3060
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3061 CAGTGTAGAATTCAGGACCAAGGCTGGGCGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
702 CAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 643
3121 TTGTTGGCTGAGGAGGAGTGTAGATTTTCTGAGGCTCAGGAGTTTCTGAGACAGCTTTGGCCAA 3180
642 TTAATACTAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 583
3181 TGGTGAACCCCATGCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 3240
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3241 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGGTGAGG 3300
522 ATAATCCCAAAATTTTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 463
3301 TTGAGTGTAGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
462 TTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 403
3361 CTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 3420
402 CTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 343
3421 TCTAATTTGCTGAGCAGCAACCTCCTGAGTTCACTACCAATGCTAGAGGTAGACACCTTAA 3480
342 TCTAATTTACCTTAAACCAACCACTCCTTAAATTTCACTACCAATGCTAGAGGTAGACACCTTAA 283


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/ PRIOR APPLICATION NUMBER: 60/218,290
/ PRIOR FILING DATE: 2000-07-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 4031
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3112
/ LENGTH: 5749
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1222)
/ OTHER INFORMATION: n equals a.t.g, or c
US-10-242-515-3112

Query Match      20.0%; Score 998.4; DB 17; Length 5749;
Best Local Similarity 99.9%; Pred. No. 8.1e-259;
Matches 999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4001 ATGGAATAATCACAAACACAGCAAGGATATGTGAGAGGGGGCTCACCTTCTCTGAGGTTG 4060
DB 1 ATGGAATAATCACAAACACAGCAAGGATATGTGAGAGGGGGCTCACCTTCTCTGAGGTTG 60

QY 4061 TCAGAGCTTTTCATCTTTTCATGTCATCTTGAAGAAACAGCTGGAAGTCTGAGGTTCTGT 4120
DB 61 TCAGAGCTTTTCATCTTTTCATGTCATCTTGAAGAAACAGCTGGAAGTCTGAGGTTCTGT 120

QY 4121 GGGAGCAGGAGAGAGGAGGATTTGCTTCTGAGATCATTTGCTTCTGGGATGTTG 4180
DB 121 GGGAGCAGGAGAGAGGAGGATTTGCTTCTGAGATCATTTGCTTCTGGGATGTTG 180

QY 4181 GAAATAGGGACCTATTCTCTTTGTTGCTGAGTTAAACAGGCTGGGATTTTTCAGAGTCCC 4240
DB 181 GAAATAGGGACCTATTCTCTTTGTTGCTGAGTTAAACAGGCTGGGATTTTTCAGAGTCCC 240

QY 4241 ACACCTCGAGGTCATCTCGGGCTGTGAAATGCAAGAACACAGTACCGAGGGCTACT 4300
DB 241 ACACCTCGAGGTCATCTCGGGCTGTGAAATGCAAGAACACAGTACCGAGGGCTACT 300

QY 4301 GGAAGTACGGGTATGATGGCAGGACCTTCAATTTCTGCTTGCCTGCACACATGGATTGA 4360
DB 301 GGAAGTACGGGTATGATGGCAGGACCTTCAATTTCTGCTTGCCTGCACACATGGATTGA 360

QY 4361 GAGCAGCAGAACCCAGGGGCTTGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTTCGGG 4420
DB 361 GAGCAGCAGAACCCAGGGGCTTGCCCAACCAAGCTGGAGTGGGAAGGCAAGATTTCGGG 420

QY 4421 CCAGGCAGAACAGGGCTTACCTGGAGAGGACTGCGCTGCACAGCTGCAGAGTTGCTGG 4480
DB 421 CCAGGCAGAACAGGGGCTTACCTGGAGAGGACTGCGCTGCACAGCTGCAGAGTTGCTGG 480

QY 4481 AGCTGGGAGAGGTGTTTGGACCAACAGATGATGGTGAACACACTTCTGCCCCCTATA 4540
DB 481 AGCTGGGAGAGGTGTTTGGACCAACAGATGATGGTGAACACACTTCTGCCCCCTATA 540

QY 4541 CTCTAGTGCAGAGTGGAGAGGTGTCAGGGCAACGGAATCCCTGGTTGGAGTTTCAGAGG 4600
DB 541 CTCTAGTGCAGAGTGGAGAGGTGTCAGGGCAACGGAATCCCTGGTTGGAGTTTCAGAGG 600

QY 4601 TGGCTGAGGCTGTGTCCTCTCCAAATTCCTGGGAAGGGAATTTCTCAATCTTAGAGTCTC 4660
DB 601 TGGCTGAGGCTGTGTCCTCTCCAAATTCCTGGGAAGGGAATTTCTCAATCTTAGAGTCTC 660

QY 4661 TACCTTATAATTTGAGATGATGAGCAGGCCAAGTCATGGGTTAAATTTCTTTTCTCCA 4720
DB 661 TACCTTATAATTTGAGATGATGAGCAGGCCAAGTCATGGGTTAAATTTCTTTTCTCCA 720

QY 4721 TGCATATGGCTCAAAGGGAAGTGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTT 4780
DB 721 TGCATATGGCTCAAAGGGAAGTGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTT 780

QY 4781 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGGCAACGCTGGCTCACCCC 4840
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DB 781 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGGCAACGCTGGCTCACCCC 840
QY 4841 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGGCAACGCTGGCTGGAGACC 4900
DB 841 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGGCAACGCTGGAGACC 900
QY 4901 AGCCTGACCAACATGTTGAAACCCGCTCTCTTAAAAAATACAAAAATTAGCTGTACAGT 4960
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; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10129
; LENGTH: 500
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: NT HIT: U91328.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q30201, EVALUE 1.00e-52
; OTHER INFORMATION: EST_HUMAN HIT: BG747345.1, EVALUE 0.00e+00
US-10-029-386-10129

Query Match      10.0%; Score 500; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.2e-124;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4129 GGAAGAGGGAAGGAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGGTGGAAATAGG 4188
DB 1 GGAAGAGGGAAGGAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGGTGGAAATAGG 60

QY 4189 GACCTATTCTTTTGGTTGTCAGTTAAACAAGGCTGGGGATTTTTCCAGAGTCCACACCCCTG 4248
DB 61 GACCTATTCTTTTGGTTGTCAGTTAAACAAGGCTGGGGATTTTTCCAGAGTCCACACCCCTG 120

QY 4249 CAGGTCATCTTGGGCTGTGAAATGCAAGAAGCAACAGTACCAGAGGCTACTTGGAAAGTAC 4308
DB 121 CAGGTCATCTTGGGCTGTGAAATGCAAGAAGCAACAGTACCAGAGGCTACTTGGAAAGTAC 180

QY 4309 GGGTATGATGGCAGGACCACTTGAATTTCTGCCCTGACACACTGATTTGGAGAGCAGCA 4368
DB 181 GGGTATGATGGCAGGACCACTTGAATTTCTGCCCTGACACACTGATTTGGAGAGCAGCA 240

QY 4369 GAACCCAGGGCTTGGCCCCACCAAGCTGGAGTGGGAAAGGCAACAAGATTGGGCCAGGCGAG 4428
DB 241 GAACCCAGGGCTTGGCCCCACCAAGCTGGAGTGGGAAAGGCAACAAGATTGGGCCAGGCGAG 300

QY 4429 AACAGGGCTTACCTGGAGAGGACCTGCCCTGACAGCTGCAGCAGTTGCTGGAGCTGGGG 4488
DB 301 AACAGGGCTTACCTGGAGAGGACCTGCCCTGACAGCTGCAGCAGTTGCTGGAGCTGGGG 360
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Qy	4489	AGAGGTGTTTGGACCAACAAGGTATGGTGGAAACACACACTTCTGCCCTATACTCTAGTG	4548
Db	361		
		AGAGGTGTTTGGACCAACAAGGTATGGTGGAAACACACACTTCTGCCCTATACTCTAGTG	420
Qy	4549	GCAGAGTGGAGGAGGTTGCAGGGCACGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAG	4608
Db	421		
		GCAGAGTGGAGGAGGTTGCAGGGCACGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAG	480
Qy	4609	GCTGTGTCCTCTCCAAATT	4628
Db	481		
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Job time : 2901.98 secs